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OM protein - protein search, using sw model

Run on: December 3, 2002, 14:35:53 ; Search time 35 seconds  
(without alignments)  
612.953 Million cell updates/sec

Title: US-09-907-263-2

Perfect score: 941

Sequence: 1 DSVCPQKXHYHPQNNISCTT.....CSNCKSLEKLCLEPQIEN 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq 101002.\*

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- 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 941   | 100.0       | 161    | 13 | Native 30 kD TNF i |
| 2          | 941   | 100.0       | 161    | 19 | Human soluble tumo |
| 3          | 941   | 100.0       | 161    | 19 | Soluble tumour nec |
| 4          | 941   | 100.0       | 161    | 20 | Tumour necrosis in |
| 5          | 941   | 100.0       | 161    | 22 | Human 30 kDa TNF i |
| 6          | 941   | 100.0       | 211    | 20 | Tumour necrosis fa |
| 7          | 941   | 100.0       | 280    | 22 | Tnf1 protein. Un   |
| 8          | 941   | 100.0       | 309    | 16 | TNF-R-GBPH fusion  |
| 9          | 941   | 100.0       | 311    | 20 | Tumour necrosis fa |
| 10         | 941   | 100.0       | 336    | 18 | TBP(20-190)/hCG-be |

|    |       |       |      |    |          |                    |
|----|-------|-------|------|----|----------|--------------------|
| 11 | 941   | 100.0 | 366  | 20 | AAW89228 | Tumour necrosis fa |
| 12 | 941   | 100.0 | 371  | 11 | AAW89229 | Tumour Necrosis Fa |
| 13 | 941   | 100.0 | 397  | 20 | AAW89227 | Tumour necrosis fa |
| 14 | 941   | 100.0 | 417  | 20 | AAW89226 | Tumour necrosis fa |
| 15 | 941   | 100.0 | 420  | 20 | AAW89224 | Tumour necrosis fa |
| 16 | 941   | 100.0 | 451  | 16 | AAW70107 | TNF-R-GBP 130 fusi |
| 17 | 941   | 100.0 | 455  | 12 | AAW10986 | 30kD TNF inhibitor |
| 18 | 941   | 100.0 | 455  | 12 | AAW11082 | Human 55kD TNF-bin |
| 19 | 941   | 100.0 | 455  | 13 | AAW20787 | TNF-alpha binding  |
| 20 | 941   | 100.0 | 455  | 13 | AAW24000 | TNF-alpha 55kD rec |
| 21 | 941   | 100.0 | 455  | 14 | AAW24059 | Lambda derived TNF |
| 22 | 941   | 100.0 | 455  | 16 | AAW75084 | p55 TNF-R. Homo s  |
| 23 | 941   | 100.0 | 455  | 20 | AAW30934 | Human tumour necro |
| 24 | 941   | 100.0 | 455  | 21 | AAW36266 | Human tumour necro |
| 25 | 941   | 100.0 | 455  | 21 | AAW37800 | Human tumour necro |
| 26 | 941   | 100.0 | 455  | 21 | AAW28984 | Human tumour necro |
| 27 | 941   | 100.0 | 455  | 21 | AAW23446 | Human TNFR 1. Hom  |
| 28 | 941   | 100.0 | 455  | 21 | AAW01336 | Human tumour necro |
| 29 | 941   | 100.0 | 455  | 22 | AAW86817 | TNF-R-GBP 130 fusi |
| 30 | 941   | 100.0 | 455  | 22 | AAW36697 | TNF-R-GBP 130 fusi |
| 31 | 941   | 100.0 | 455  | 22 | AAW37677 | TNF-R-GBP 130 fusi |
| 32 | 941   | 100.0 | 455  | 23 | ABW81649 | TNF-R-GBP 130 fusi |
| 33 | 941   | 100.0 | 455  | 23 | AAU75064 | TNF-R-GBP 130 fusi |
| 34 | 941   | 100.0 | 455  | 23 | AAW70104 | TNF-R-GBP 130 fusi |
| 35 | 941   | 100.0 | 884  | 16 | AAW70109 | TNF-R-GBP 130 fusi |
| 36 | 941   | 100.0 | 900  | 16 | AAW70103 | TNF-R-GBP 130 fusi |
| 37 | 941   | 100.0 | 1245 | 16 | AAW70106 | TNF-R-Pl. Vivax Du |
| 38 | 941   | 100.0 | 1604 | 16 | AAW70105 | TNF-R-EBA 175 fusi |
| 39 | 938   | 99.7  | 455  | 11 | AAW07451 | Human Tumour Necro |
| 40 | 932   | 99.0  | 433  | 14 | AAW51032 | Mutant p55 tumour  |
| 41 | 932   | 99.0  | 443  | 14 | AAW51033 | Mutant p55 tumour  |
| 42 | 932   | 99.0  | 455  | 14 | AAW42197 | p55 Tumour necrosi |
| 43 | 932   | 99.0  | 455  | 14 | AAW51034 | Mutant p55 tumour  |
| 44 | 931   | 98.9  | 455  | 12 | AAW12550 | Type I TNF recepto |
| 45 | 930.5 | 98.9  | 909  | 19 | AAW64485 | Human Fas protein. |

ALIGNMENTS

RESULT 1  
AAW27496  
ID AAR27496 standard; protein; 161 AA.

XX AAR27496;

XX 09-MAR-1993 (first entry)

XX Native 30 kD TNF inhibitor.

XX Tumour necrosis factor; ethylene glycol; pharmacokinetic;  
XX adult respiratory distress syndrome; rheumatoid arthritis;  
XX septic shock; pulmonary fibrosis; spacer.

OS Homo sapiens.

XX WO9216221-A.

XX 01-OCT-1992.

XX 13-MAR-1992; 92WO-US02122.

XX 15-MAR-1991; 91US-0659862.

XX 17-JAN-1992; 92US-0822296.

XX (SYND ) SYNERGEN INC.

XX Armes LG, Brewer MT, Evans RJ, Kohno T, Thompson RC;

XX WPI; 1992-348933/42.

XX New ethylene glycolated polypeptide(s) with improved  
XX pharmacokinetic properties - for treating e.g. TNF and IL-1

PT mediated diseases, e.g. adult respiratory distress syndrome,  
PT rheumatoid arthritis, septic shock etc.

PS Claim 54; Fig 2; 100pp; English.

XX The sequence shows a native 30 kD TNF inhibitor which may be  
CC modified to contain at least one non-native cysteine residue, pref.  
CC at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is  
CC joined to a non-peptidic polymer, pref. monomethoxy PEG via  
CC this non-peptidic spacer. Two such TNF inhibitor mols. may be linked via  
CC pharmacokinetic properties, i.e. increased mol. wt. hence reduced  
CC clearance rate following s.c. or systemic administration, increased  
CC sol. of native TNF inhibitors, and reduced antigenicity. The  
CC polypeptides may be used for treatment of TNF mediated diseases such  
CC as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid  
CC arthritis, inflammatory bowel disease and septic shock. The same  
CC method may be applied to the interleukin-1 receptor antagonist  
CC IL-1ra. See also AAR27495.

XX Sequence 161 AA;

Query Match 100.0%; Score 941; DB 13; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.4e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPNNSICTCKCHKGTLYLNDPCPGQDPTDCRECSGSFTASENHLRHCL 60  
Db 1 DSVCPQGYIHPNNSICTCKCHKGTLYLNDPCPGQDPTDCRECSGSFTASENHLRHCL 60

Qy 61 SCSKCRKEMGVEIISCTVDRDVTGCGCRKNQYRHYSENLFQCFNCSCLNGTVHLSQOE 120  
Db 61 SCSKCRKEMGVEIISCTVDRDVTGCGCRKNQYRHYSENLFQCFNCSCLNGTVHLSQOE 120

Qy 121 KONTVCTCHAGFPLENECVSCSNCKSKLECKTCLPQIEN 161  
Db 121 KONTVCTCHAGFPLENECVSCSNCKSKLECKTCLPQIEN 161

#### RESULT 2

AAW59664  
ID AAW59664 standard; Protein; 161 AA.

XX AAW59664;

DT 28-SEP-1998 (first entry)

DE Human soluble tumour necrosis factor receptor type I.

XX Human; tumour necrosis factor; TNF; TNF receptor type I;

KW inflammatory disease; leukaemia; TNF binding protein;  
KW anti-inflammatory drug; methotrexates.

XX Homo sapiens.

XX WO9824463-A2.

XX 11-JUN-1998.

XX 08-DEC-1997; 97WO-US22733.

XX 09-JUL-1997; 97US-0052023.

XX 06-DEC-1996; 96US-0032587.

XX 23-JAN-1997; 97US-0036355.

XX 07-FEB-1997; 97US-0039315.

XX (AMGE-) AMGEN INC.

XX Bendele AM, Edwards CK, Sennello RM;  
XX MPI, 1998-333039/29.  
XX N-PSDB; AAV41548.

PT Treatment of acute or chronic inflammatory disease, e.g. leukaemia -  
PT by administering tumour necrosis factor binding protein and at least  
PT one additional anti-inflammatory drug, e.g. methotrexate

PS Disclosure; Fig 1; 104pp; English.

XX This is the amino acid sequence of the human tumour necrosis factor  
CC receptor type I, used in the method of the invention involving the  
CC treatment of acute or chronic inflammatory disease such as leukaemia  
CC by administering tumour necrosis factor binding protein and at least  
CC one additional anti-inflammatory drug, e.g. methotrexate.

XX Sequence 161 AA;

Query Match 100.0%; Score 941; DB 19; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.4e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPNNSICTCKCHKGTLYLNDPCPGQDPTDCRECSGSFTASENHLRHCL 60  
Db 1 DSVCPQGYIHPNNSICTCKCHKGTLYLNDPCPGQDPTDCRECSGSFTASENHLRHCL 60

Qy 61 SCSKCRKEMGVEIISCTVDRDVTGCGCRKNQYRHYSENLFQCFNCSCLNGTVHLSQOE 120  
Db 61 SCSKCRKEMGVEIISCTVDRDVTGCGCRKNQYRHYSENLFQCFNCSCLNGTVHLSQOE 120

Qy 121 KONTVCTCHAGFPLENECVSCSNCKSKLECKTCLPQIEN 161  
Db 121 KONTVCTCHAGFPLENECVSCSNCKSKLECKTCLPQIEN 161

#### RESULT 3

AAW52267  
ID AAW52267 standard; Protein; 161 AA.

XX AAW52267;

DT 29-JUN-1998 (first entry)

DE Soluble tumour necrosis factor receptor.

XX Soluble tumour necrosis factor receptor; sTNFR; TNF-mediated disease;

KW tumour necrosis factor binding protein; autoimmune disease; arthritis;

KW adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy;

KW chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNBP.

XX Homo sapiens.

XX WO9801555-A2.

XX 15-JAN-1998.

XX 09-JUL-1997; 97WO-US12244.

XX 04-MAR-1997; 97US-0037992.

XX 09-JUL-1996; 96US-0021443.

XX 06-DEC-1996; 96US-0032534.

XX 23-JAN-1997; 97US-0037737.

XX 07-FEB-1997; 97US-0039314.

XX (AMGE-) AMGEN INC.

XX Edwards CK, Fisher EF, Kieft GL;  
XX MPI, 1998-101052/09.  
XX N-PSDB; AAV19801.

XX Truncated and soluble forms of tumour necrosis factor receptor -  
XX useful for treating diseases involving factor, e.g. arthritis and  
XX adult respiratory distress syndrome  
XX Claim 1; Fig 1; 205pp; English.

This sequence is the human soluble tumour necrosis factor receptor (sTNFR). The protein was used to make the truncated sTNFR proteins of the invention. The truncated sTNFR proteins and tumour necrosis factor binding proteins (TNBP) are used to treat any TNF-mediated disease, e.g. arthritis, adult respiratory distress syndrome, cachexia/anorexia, cancer, chronic fatigue syndrome, graft rejection, Alzheimer's disease and other autoimmune diseases. Cells transformed with a vector containing DNA encoding the protein may be used for production of recombinant sTNFR, which may also be used for measuring the amount of sTNFR in samples and to raise antibodies against sTNFR. TNBP may also be used in preparation of therapeutic compositions for treating the above diseases. The sTNFR proteins are well suited to large scale production (since they lack the dematination site in region 111-126, so are more stable in vivo); contain fewer disulphide bonds and fewer epitopes, making them less antigenic than full-length proteins.

Sequence 161 AA;

Query Match 100.0%; Score 941; DB 19; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.4e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGVYIHPQNNISICTKCHKGTLYLYNDPCPGQDTCRECSGSFTASENHLRCL 60  
DB 1 DSVCPQGVYIHPQNNISICTKCHKGTLYLYNDPCPGQDTCRECSGSFTASENHLRCL 60  
QY 61 SCSKCRKEMGQVEISSCTVDRDTVCGRKNQYRHWSENLFCFNCISLCLNGTVHLSQOE 120  
DB 61 SCSKCRKEMGQVEISSCTVDRDTVCGRKNQYRHWSENLFCFNCISLCLNGTVHLSQOE 120  
QY 121 KQNTVCTCHAGFFLENECVSCSNCKKSLCTKLCPLQIEN 161  
DB 121 KQNTVCTCHAGFFLENECVSCSNCKKSLCTKLCPLQIEN 161

RESULT 4

AAW89233

ID AAW89233 standard; Protein; 161 AA.

XX AC AAW89233;

XX DT 04-MAR-1999 (first entry)

XX DE Tumour necrosis inhibitor 30 kDa protein.

XX KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
XX KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
XX KW inflammation; apoptosis.

XX OS Homo sapiens.

XX PN WO9849305-A1.

XX PD 05-NOV-1998.

XX PF 29-APR-1998; 98WO-US08631.

XX PR 01-MAY-1997; 97US-0850188.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ, Wooden S;

XX DR WPI; 1999-034661/03.

XX DR N-PSDB; AAV81732.

XX PT New chimeric osteoprotegerin polypeptides - contain the  
XX PT osteoprotegerin dimerisation domain and a heterologous sequence,  
XX PT useful to treat TNF and TNFR-mediated disorders

XX PS Disclosure; Fig 2; 92pp; English.

XX CC The present invention describes a chimeric polypeptide (A1), comprising

CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
CC amino acid sequence. Also described are: (1) a multimer polypeptide  
CC comprising covalently associated Al monomers; (2) an isolated nucleic  
CC acid encoding Al; (3) an expression vector comprising the nucleic acid  
CC sequence; and (4) a host cell transformed or transfected with the  
CC expression vector so that the nucleic acid is expressible. The products  
CC from the present invention are useful to treat a variety of disorders  
CC including those related to receptor binding. Compositions comprising  
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
CC autoimmune diseases and disorders related to excessive apoptosis. The  
CC chimeras are also useful for detecting molecules which interact with  
CC fused heterologous sequences to identify potential new receptors and  
CC ligands. The present sequence represents the TNF inhibitor 30 kDa  
CC protein.

XX SQ Sequence 161 AA;

Query Match 100.0%; Score 941; DB 20; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.4e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGVYIHPQNNISICTKCHKGTLYLYNDPCPGQDTCRECSGSFTASENHLRCL 60  
DB 1 DSVCPQGVYIHPQNNISICTKCHKGTLYLYNDPCPGQDTCRECSGSFTASENHLRCL 60  
QY 61 SCSKCRKEMGQVEISSCTVDRDTVCGRKNQYRHWSENLFCFNCISLCLNGTVHLSQOE 120  
DB 61 SCSKCRKEMGQVEISSCTVDRDTVCGRKNQYRHWSENLFCFNCISLCLNGTVHLSQOE 120  
QY 121 KQNTVCTCHAGFFLENECVSCSNCKKSLCTKLCPLQIEN 161  
DB 121 KQNTVCTCHAGFFLENECVSCSNCKKSLCTKLCPLQIEN 161

RESULT 5

AAW37676

ID AAW37676 standard; protein; 161 AA.

XX AC AAW37676;

XX DT 02-MAR-2001 (first entry)

XX DE Human 30 kDa TNF inhibitor.

XX KW TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;  
XX KW IL-1; inflammatory disease; degenerative disease; human.

XX OS Homo sapiens.

XX PN US6143866-A.

XX PD 07-NOV-2000.

XX PF 19-JAN-1995; 95US-0375242.

XX PR 19-JUL-1990; 90US-0555274.

XX PR 09-JUL-1993; 93US-0090366.

XX PR 18-JUL-1989; 89US-0381080.

XX PR 11-DEC-1989; 89US-0450329.

XX PR 07-FEB-1990; 90US-0479661.

XX PA (AMGE-) AMGEN INC.

XX PI Squires C, King MW, Hale KK, Brewer MT, Thompson RC;

XX PI Vanderslice RW, Vannice J, Kohno T;

XX DR WPI; 2001-006443/01.

XX DR N-PSDB; AAC83945.

XX PT Novel 30 kDa tumor necrosis factor inhibitor analog comprising a  
XX PT non-native cysteine residue cross-linked with polyethylene glycol,  
XX PT useful for treating inflammatory and degenerative diseases mediated by

PT TNF -  
 XX Claim 1, Fig 19, 82pp; English.  
 XX  
 CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors  
 CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The  
 CC novel TNF inhibitors of the present invention are useful as therapeutic  
 CC agents for inhibiting the activity of TNF and interleukin (IL-1), and  
 CC for treating inflammatory and degenerative diseases mediated by TNF. The  
 CC 30 kDa TNF inhibitor can inhibit TNF alpha.  
 CC  
 XX  
 SQ Sequence 161 AA;  
 Query Match 100.0%; Score 941; DB 22; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-67;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSVCPQGYIHPONNSICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRHCL 60  
 Db 1 DSVCPQGYIHPONNSICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRHCL 60  
 QY 61 SCSKCRKEMGVEISSCTVDRDVTVCGRKQYRHYWSENLFQCTNCSLCINGTVHLSOE 120  
 Db 61 SCSKCRKEMGVEISSCTVDRDVTVCGRKQYRHYWSENLFQCTNCSLCINGTVHLSOE 120  
 QY 121 KONTVCTCHAGFPLENECVSCSNCKSLLECTKLCPLPOIEN 161  
 Db 121 KONTVCTCHAGFPLENECVSCSNCKSLLECTKLCPLPOIEN 161  
 RESULT 6  
 AAB89225  
 ID AAB89225 standard; Protein: 211 AA.  
 XX  
 AC AAB89225;  
 XX  
 DT 04-MAR-1999 (first entry)  
 XX  
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp 4.0.  
 XX  
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO9849305-A1.  
 XX  
 PD 05-NOV-1998.  
 XX  
 PF 29-APR-1998; 98WO-US08631.  
 XX  
 PR 01-MAY-1997; 97US-0850188.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Wooden S;  
 XX  
 DR WPI; 1999-034661/03.  
 XX  
 PT New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders  
 XX  
 PS Example 1, Fig 4; 92pp; English.  
 XX  
 CC The present invention describes a chimeric polypeptide (A1), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the

CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents a TNFbp/OPG construct from  
 CC the example of the present invention for creating TNFbp/OPG fusion  
 CC proteins.  
 CC  
 XX  
 SQ Sequence 211 AA;  
 Query Match 100.0%; Score 941; DB 20; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-67;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSVCPQGYIHPONNSICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRHCL 60  
 Db 41 DSVCPQGYIHPONNSICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRHCL 100  
 QY 61 SCSKCRKEMGVEISSCTVDRDVTVCGRKQYRHYWSENLFQCTNCSLCINGTVHLSOE 120  
 Db 101 SCSKCRKEMGVEISSCTVDRDVTVCGRKQYRHYWSENLFQCTNCSLCINGTVHLSOE 160  
 QY 121 KONTVCTCHAGFPLENECVSCSNCKSLLECTKLCPLPOIEN 161  
 Db 161 KONTVCTCHAGFPLENECVSCSNCKSLLECTKLCPLPOIEN 201  
 RESULT 7  
 AAB66979  
 ID AAB66979 standard; Protein: 280 AA.  
 XX  
 AC AAB66979;  
 XX  
 DT 19-APR-2001 (first entry)  
 XX  
 DE Tnfr1 protein.  
 XX  
 KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;  
 KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;  
 KW systemic lupus erythematosus; graft-versus-host disease; septic shock;  
 KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;  
 KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;  
 KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;  
 KW ischaemia; Parkinson's disease.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200103719-A2.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 07-JUL-2000; 2000WO-US18667.  
 XX  
 PR 09-JUL-1999; 99US-0350670.  
 XX  
 PR 09-DEC-1999; 99US-0457647.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;  
 XX  
 DR WPI; 2001-103031/11.  
 XX  
 PT Treating conditions leading to bone loss such as rheumatoid arthritis,  
 PT multiple sclerosis and asthma, comprises administering an  
 PT osteoprotegerin protein in conjunction with e.g. inhibitors of  
 PT interleukin and tumor necrosis factor alpha  
 XX  
 PS Disclosure; Fig 2; 316pp; English.  
 XX

CC The present invention relates to a method for treating conditions leading  
 CC to bone loss. The method comprises administering a purified and isolated  
 CC osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)  
 CC in conjunction with other substances such as tumour necrosis factor- $\alpha$   
 CC (TNF- $\alpha$ ) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE  
 CC modulators, fibroblast growth factor (FGF)-1-10 modulators and/or platelet  
 CC activating factor (PAF) antagonists. The method is useful for treating  
 CC conditions leading to bone loss such as rheumatoid arthritis, multiple  
 CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also  
 CC useful for treating inflammation, systemic lupus erythematosus (SLE) and  
 CC graft-versus-host disease (GVHD). Other diseases that can be treated  
 CC include acute pancreatitis, Alzheimer's disease, anorexia,  
 CC atherosclerosis, coronary conditions (e.g. myocardial infarction),  
 CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,  
 CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,  
 CC psoriasis and septic shock. The present sequence was used in a sequence  
 CC homology comparison.

XX Sequence 280 AA;  
 CC Query Match 100.0%; Score 941; DB 22; Length 280;  
 CC Best Local Similarity 100.0%; Pred. No. 4e-67;  
 CC Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSVCPQGYIHPQNNISICTCKHGTLYNDPCPGQDTDCRECSGSFTASENHLRHCL 60  
 Db 41 DSVCPQGYIHPQNNISICTCKHGTLYNDPCPGQDTDCRECSGSFTASENHLRHCL 100  
 QY 61 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHWSENLFCQNCISCLNGTVHLSQOE 120  
 Db 101 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHWSENLFCQNCISCLNGTVHLSQOE 160  
 QY 121 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 161  
 Db 161 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 201

RESULT 8  
 AAR70108  
 ID AAR70108 standard; Protein; 309 AA.  
 AC AAR70108;  
 DT 10-NOV-1995 (first entry)  
 XX TNF-R-GBPH fusion protein.  
 XX Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;  
 KW red blood cell; cytokine receptor; glycoprotein binding peptide 130;  
 KW GBP 130; GBPH; glycoprotein binding peptide homologue; glycoprotein A;  
 KW tumour necrosis factor receptor; TNF-R.  
 XX Chimeric Homo sapiens.  
 OS Chimeric Plasmodium falciparum.  
 XX Key Location/Qualifiers  
 FH Misc-difference 230..269  
 FT /label= repeat region  
 FT /note= "can be repeated n times, where n is a real  
 FT number"

XX WO9506737-A.  
 FN 09-MAR-1995.  
 XX 01-SEP-1994; 94WO-GB01900.  
 XX 03-SEP-1993; 93GB-0018350.  
 XX 23-AUG-1994; 94GB-0017021.  
 XX (PREN/) PRENDERGAST K F.  
 XX Prendergast KF;  
 FI

XX WPI; 1995-115452/15.  
 DR New hybrid peptide(s) for binding cytokine(s) - comprising a  
 XX malaria parasite peptide capable of binding a red blood cell and  
 PT a receptor peptide.  
 XX Example A; Page 54-55; 93pp; English.

XX Hybrid peptides for binding cytokines, comprising a malaria parasite  
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood  
 CC cell (RBC)) and a receptor peptide are claimed. AAR70103-25 are examples  
 CC of these hybrid peptides. AAR70108 is a fusion of tumour necrosis factor  
 CC receptor (in accordance with H Loetscher et al Cell. Vol. 61, 351-359)  
 CC and glycoprotein binding protein (GBP) homologue (GBPH). The  
 CC use of cytokine receptors not normally found on RBCs means that the  
 CC cytokine can bind harmlessly to the RBC without deleterious effect.  
 CC The RBC protects the hybrid peptides from excretion from the kidney, and  
 CC due to steric hindrance prevents the cytokines binding to a receptor in  
 CC another cell. GBP 130 or GBPH are the pref. malaria parasite peptides  
 CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),  
 CC PMSA (pre major merozoite surface antigen) and the buffy binding  
 CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides  
 CC bind to pref. glycoprotein A, B and C, sialo glycoproteins, found on the  
 CC surface of RBCs. The hybrid peptides are thus used to lower the levels of  
 CC free cytokines in the circulation to reduce pathological damage.

XX Sequence 309 AA;

Query Match 100.0%; Score 941; DB 16; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-67;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSVCPQGYIHPQNNISICTCKHGTLYNDPCPGQDTDCRECSGSFTASENHLRHCL 60  
 Db 20 DSVCPQGYIHPQNNISICTCKHGTLYNDPCPGQDTDCRECSGSFTASENHLRHCL 79  
 QY 61 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHWSENLFCQNCISCLNGTVHLSQOE 120  
 Db 80 SCSKCRKEMGQVEISSCTVDRDTCGCRKNQYRHWSENLFCQNCISCLNGTVHLSQOE 139  
 QY 121 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 161  
 Db 140 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 180

RESULT 9  
 AAW89229  
 ID AAW89229 standard; Protein; 311 AA.  
 AC AAW89229;  
 XX 04-MAR-1999 (first entry)  
 DT Tumour necrosis factor bp/osteoprotegerin construct TNFbp/304.  
 DE Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO9849305-A1.  
 FN 05-NOV-1998.  
 XX 29-APR-1998; 98WO-US08631.  
 XX 01-MAY-1997; 97US-0850188.  
 XX (AMGE-) AMGEN INC.

PI Boyle WJ, Wooden S;  
XX  
DR WPI; 1999-034661/03.

XX New chimeric osteoprotegerin polypeptides - contain the  
PT osteoprotegerin dimerisation domain and a heterologous sequence,  
PT useful to treat TNF and TNFR-mediated disorders

XX Example 1; Fig 4; 92pp; English.

XX The present invention describes a chimeric polypeptide (A1), comprising  
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
CC amino acid sequence. Also described are: (1) a multimer polypeptide  
CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
CC sequence; and (4) a host cell transformed or transfected with the  
CC expression vector so that the nucleic acid is expressible. The products  
CC from the present invention are useful to treat a variety of disorders  
CC including those related to receptor binding. Compositions comprising  
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
CC autoimmune diseases and disorders related to excessive apoptosis. The  
CC chimeras are also useful for detecting molecules which interact with  
CC fused heterologous sequences to identify potential new receptors and  
CC ligands. The present sequence represents a TNFbp/OPG construct from  
CC the example of the present invention for creating TNFbp/OPG fusion  
CC proteins.

XX Sequence 311 AA;

Query Match 100.0%; Score 941; DB 20; Length 311;  
Best Local Similarity 100.0%; Pred. No. 4.4e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGGKYIHPPNNNSICTCKCHKGTLYLNDPDPGDDTCRECESSFTASENHLRHCL 60

DB 41 DSVCPQGGKYIHPPNNNSICTCKCHKGTLYLNDPDPGDDTCRECESSFTASENHLRHCL 100

QY 61 SCSKCRKEMGVEIISCTVDRDTCGCRKNQRYHWSENLFQCFNCSCLNGTVHLSQOE 120

DB 101 SCSKCRKEMGVEIISCTVDRDTCGCRKNQRYHWSENLFQCFNCSCLNGTVHLSQOE 160

QY 121 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCLEPIEN 161

DB 161 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCLEPIEN 201

RESULT 10  
AAW33360  
ID AAW33360 standard; Protein; 336 AA.

XX AAW33360;

XX 19-MAR-1998 (first entry)

XX TBP(20-190)/hCG-beta fusion protein.

XX Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;

KW beta subunit; hCG-beta.

XX Homo sapiens.

XX MO9730161-A1.

XX 21-AUG-1997.

XX 20-FEB-1997; 97WO-US02315.

XX 20-FEB-1996; 96US-0011936.

XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Campbell RK, Chapel SC, Jameson BA;

XX WPI; 1997-425036/39.  
DR N-PSDB; AAT94022.

XX Hybrid dimeric protein comprising two co-expressed units - each  
PT based on receptor or ligand and a subunit of a heterodimeric  
PT hormone, especially FSH, for inducing follicular maturation

XX Example; Pages 39-40; 60pp; English.

XX A novel fusion protein comprises 2 dimer forming co-expressed amino  
CC acid sequences, each consisting of a homodimeric or heterodimeric  
CC receptor chain or ligand, with ligand-receptor binding activity,  
CC bound directly or via a peptide linker to a subunit of a  
CC heterodimeric protein hormone capable of forming a heterodimer with  
CC the hormone's other subunits. The fusion protein, e.g. the  
CC thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit  
CC (hCG-beta) fusion protein denoted by the present sequence,  
CC significantly increases the biological activity of the hormone  
CC component, reducing the requirement for hormone itself and the  
CC number of injections needed.

XX Sequence 336 AA;

Query Match 100.0%; Score 941; DB 18; Length 336;  
Best Local Similarity 100.0%; Pred. No. 4.7e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGGKYIHPPNNNSICTCKCHKGTLYLNDPDPGDDTCRECESSFTASENHLRHCL 60

DB 23 DSVCPQGGKYIHPPNNNSICTCKCHKGTLYLNDPDPGDDTCRECESSFTASENHLRHCL 82

QY 61 SCSKCRKEMGVEIISCTVDRDTCGCRKNQRYHWSENLFQCFNCSCLNGTVHLSQOE 120

DB 83 SCSKCRKEMGVEIISCTVDRDTCGCRKNQRYHWSENLFQCFNCSCLNGTVHLSQOE 142

QY 121 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCLEPIEN 161

DB 143 KONTVCTCHAGFFLENECVSCSNCKSLLECTKLCLEPIEN 193

RESULT 11  
AAM89228

ID AAM89228 standard; Protein; 366 AA.

XX AAM89228;

XX 04-MAR-1999 (first entry)

XX Tumour necrosis factor bp/osteoprotegerin construct TNFbp/248.

XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;

KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;

XX inflammation; apoptosis.

XX Homo sapiens.

XX Synthetic.

XX WO9849305-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US08631.

XX 01-MAY-1997; 97US-0850188.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Wooden S;

XX WPI; 1999-034661/03.

XX New chimeric osteoprotegerin polypeptides - contain the

PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 XX useful to treat TNF and TNFR-mediated disorders  
 PS Example 1; Fig 4; 92pp; English.  
 XX  
 CC The present invention describes a chimeric polypeptide (A1), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the  
 CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents a TNFbp/OPG construct from  
 CC the example of the present invention for creating TNFbp/OPG fusion  
 CC proteins.  
 XX  
 SQ Sequence 365 AA;  
 Query Match 100.0%; Score 941; DB 20; Length 365;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-67;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRCL 60  
 DB 41 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRCL 100  
 QY 61 SCSKCRKEMGOVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSOE 120  
 DB 101 SCSKCRKEMGOVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSOE 160  
 QY 121 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 161  
 DB 161 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 201  
 RESULT 12  
 AAR07449  
 ID AAR07449 standard; protein; 371 AA.  
 XX  
 AC AAR07449;  
 XX  
 DT 29-JAN-1991 (first entry)  
 XX  
 DE Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.  
 XX  
 KW Tumour necrosis factor binding protein; TNF-BP; TNF receptor;  
 KW pTNF-BP15; infectious disease; parasitic disease; cachexia;  
 KW autoimmune disease; shock.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP393438-A.  
 XX  
 PD 24-OCT-1990.  
 XX  
 PF 06-APR-1990; 90EP-0106624.  
 XX  
 PR 21-JUN-1989; 89DE-3920282.  
 PR 21-APR-1989; 89DE-3913101.  
 XX  
 PA (BOEH ) BOEHRINGER INGELHEIMINT.  
 XX  
 PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;  
 XX  
 DR WPI; 1990-321987/43.  
 DR N-PSDB; AAQ06282.

XX DNA encoding TNF binding protein and TNF- receptor - used in  
 PT tumour treatment and to understand mechanism to TNF action  
 XX  
 PS Disclosure; Fig 1(1-3); 51pp; German.  
 XX  
 CC Clone pTNF-BP15 was used to construct PADTNF-BP, for transfection of  
 CC e.g. COS7 cells. The expressed proteins are useful  
 CC prophylactically and therapeutically to control disorders which  
 CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or  
 CC parasitic diseases, shock, cachexia, autoimmune diseases, adult  
 CC respiratory distress syndrome etc., or side effects of treatment with  
 CC TNF-alpha). They can also be used as diagnostic reagents for  
 CC assaying TNF and in study of TNF-receptor interactions.  
 CC See also AAQ06282-Q06285.  
 XX  
 SQ Sequence 371 AA;  
 Query Match 100.0%; Score 941; DB 11; Length 371;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-67;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRCL 60  
 DB 41 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRCL 100  
 QY 61 SCSKCRKEMGOVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSOE 120  
 DB 101 SCSKCRKEMGOVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSOE 160  
 QY 121 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 161  
 DB 161 KQNTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 201  
 RESULT 13  
 AAW89227  
 ID AAW89227 standard; Protein; 397 AA.  
 XX  
 AC AAW89227;  
 XX  
 DT 04-MAR-1999 (first entry)  
 XX  
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/217.  
 XX  
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO9849305-A1.  
 XX  
 PD 05-NOV-1998.  
 XX  
 PF 29-APR-1998; 98WO-US08631.  
 XX  
 PR 01-MAY-1997; 97US-0850188.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Wooden S;  
 XX  
 DR WPI; 1999-034661/03.  
 XX  
 PT New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders  
 XX  
 PS Example 1; Fig 4; 92pp; English.  
 XX  
 CC The present invention describes a chimeric polypeptide (A1), comprising

CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
CC amino acid sequence. Also described are: (1) a multimer polypeptide  
CC comprising covalently associated Al monomers; (2) an isolated nucleic  
CC acid encoding Al; (3) an expression vector comprising the nucleic acid  
CC sequence; and (4) a host cell transformed or transfected with the  
CC expression vector so that the nucleic acid is expressible. The products  
CC from the present invention are useful to treat a variety of disorders  
CC including those related to receptor binding. Compositions comprising  
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
CC autoimmune diseases and disorders related to excessive apoptosis. The  
CC chimeras are also useful for detecting molecules which interact with  
CC fused heterologous sequences to identify potential new receptors and  
CC ligands. The present sequence represents a TNFbp/OPG construct from  
CC the example of the present invention for creating TNFbp/OPG fusion  
CC proteins.

XX Sequence 397 AA;

Query Match 100.0%; Score 941; DB 20; Length 397;  
Best Local Similarity 100.0%; Pred. No. 5,5e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQKGIHPQNNISICTCKHGTLYLNDPCPGQDTCREBSGSFTASENHLRHCL 60  
Db 41 DSVCPQKGIHPQNNISICTCKHGTLYLNDPCPGQDTCREBSGSFTASENHLRHCL 100

QY 61 SCSKCRKEMGVEIISCTVDRDTCGCRKNQYRHWSENLFCQFNCSLCLNGTVHLSQOE 120  
Db 101 SCSKCRKEMGVEIISCTVDRDTCGCRKNQYRHWSENLFCQFNCSLCLNGTVHLSQOE 160

QY 121 KONTVCTCHAGFFLRENECVSCSNCKSLLECTKLCPLPIEN 161  
Db 161 KONTVCTCHAGFFLRENECVSCSNCKSLLECTKLCPLPIEN 201

RESULT 14  
AAW89226  
ID AAW89226 standard; Protein; 417 AA.

XX AAW89226;

DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/196.

XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
KM inflammation; apoptosis.

XX Homo sapiens.  
OS Synthetic.

XX WO9849305-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US08631.

XX 01-MAY-1997; 97US-0850188.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Wooden S;

XX WPI; 1999-034661/03.

XX New chimeric osteoprotegerin polypeptides - contain the  
PT osteoprotegerin dimerisation domain and a heterologous sequence,  
PT useful to treat TNF and TNFR-mediated disorders

XX Example 1, Fig 4, 92pp; English.

CC The present invention describes a chimeric polypeptide (A1), comprising  
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
CC amino acid sequence. Also described are: (1) a multimer polypeptide  
CC comprising covalently associated Al monomers; (2) an isolated nucleic  
CC acid encoding Al; (3) an expression vector comprising the nucleic acid  
CC sequence; and (4) a host cell transformed or transfected with the  
CC expression vector so that the nucleic acid is expressible. The products  
CC from the present invention are useful to treat a variety of disorders  
CC including those related to receptor binding. Compositions comprising  
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
CC autoimmune diseases and disorders related to excessive apoptosis. The  
CC chimeras are also useful for detecting molecules which interact with  
CC fused heterologous sequences to identify potential new receptors and  
CC ligands. The present sequence represents a TNFbp/OPG construct from  
CC the example of the present invention for creating TNFbp/OPG fusion  
CC proteins.

XX Sequence 417 AA;

Query Match 100.0%; Score 941; DB 20; Length 417;  
Best Local Similarity 100.0%; Pred. No. 5,8e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQKGIHPQNNISICTCKHGTLYLNDPCPGQDTCREBSGSFTASENHLRHCL 60  
Db 41 DSVCPQKGIHPQNNISICTCKHGTLYLNDPCPGQDTCREBSGSFTASENHLRHCL 100

QY 61 SCSKCRKEMGVEIISCTVDRDTCGCRKNQYRHWSENLFCQFNCSLCLNGTVHLSQOE 120  
Db 101 SCSKCRKEMGVEIISCTVDRDTCGCRKNQYRHWSENLFCQFNCSLCLNGTVHLSQOE 160

QY 121 KONTVCTCHAGFFLRENECVSCSNCKSLLECTKLCPLPIEN 161  
Db 161 KONTVCTCHAGFFLRENECVSCSNCKSLLECTKLCPLPIEN 201

RESULT 15  
AAW89224  
ID AAW89224 standard; Protein; 420 AA.

XX AAW89224;

DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/OPG.

XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
KM inflammation; apoptosis.

XX Homo sapiens.  
OS Synthetic.

XX WO9849305-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US08631.

XX 01-MAY-1997; 97US-0850188.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Wooden S;

XX WPI; 1999-034661/03.

XX New chimeric osteoprotegerin polypeptides - contain the  
PT osteoprotegerin dimerisation domain and a heterologous sequence,  
PT useful to treat TNF and TNFR-mediated disorders

XX Example 1, Fig 4, 92pp; English.



XX The present invention describes a chimeric polypeptide (A1), comprising  
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
CC amino acid sequence. Also described are: (1) a multimer polypeptide  
CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
CC sequence; and (4) a host cell transformed or transfected with the  
CC expression vector so that the nucleic acid is expressible. The products  
CC from the present invention are useful to treat a variety of disorders  
CC including those related to receptor binding. Compositions comprising  
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
CC autoimmune diseases and disorders related to excessive apoptosis. The  
CC chimeras are also useful for detecting molecules which interact with  
CC fused heterologous sequences to identify potential new receptors and  
CC ligands. The present sequence represents a TNFbp/OPG construct from  
CC the example of the present invention for creating TNFbp/OPG fusion  
CC proteins.  
XX

SQ Sequence 420 AA;

Query Match 100.0%; Score 941; DB 20; Length 420;  
Best Local Similarity 100.0%; Pred. No. 5.8e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DSVCPQGYIHPQNNISICTKCHKGTLYLNDPCPGQDTDCRECSGSFTASENHLRHCL 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
41 DSVCPQGYIHPQNNISICTKCHKGTLYLNDPCPGQDTDCRECSGSFTASENHLRHCL 100  
QY 61 SCSKCRKEMQVEISSCTVDRDTCGCRKQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
101 SCSKCRKEMQVEISSCTVDRDTCGCRKQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 160  
QY 121 KQNTVCTCHAGFFLRENECVSCNCKKSLECTKLCPLQIEN 161  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
161 KQNTVCTCHAGFFLRENECVSCNCKKSLECTKLCPLQIEN 201

Search completed: December 3, 2002, 14:40:05  
Job time : 37 secs



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OM protein - protein search, using sw model

Run on: December 3, 2002, 14:39:28 ; Search time 15 Seconds  
(without alignments)  
315.806 Million cell updates/sec

Title: US-09-907-263-2  
Perfect score: 941  
Sequence: 1 DSVCPQKVIHPQNSICCT.....CSNCKSLSECTKLCIPQIEN 161

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/6C COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/6D COMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 941   | 100.0       | 161    | 4  | US-09-326-394-2    |
| 2          | 941   | 100.0       | 280    | 3  | US-08-974-022-46   |
| 3          | 941   | 100.0       | 280    | 4  | US-08-795-445A-46  |
| 4          | 941   | 100.0       | 280    | 4  | US-08-795-447A-46  |
| 5          | 941   | 100.0       | 280    | 4  | US-08-974-186-46   |
| 6          | 941   | 100.0       | 280    | 4  | US-08-795-446B-46  |
| 7          | 941   | 100.0       | 280    | 4  | US-08-706-945D-132 |
| 8          | 941   | 100.0       | 336    | 4  | US-08-804-166-8    |
| 9          | 941   | 100.0       | 336    | 4  | US-08-910-991-8    |
| 10         | 941   | 100.0       | 455    | 1  | US-08-050-319B-25  |
| 11         | 941   | 100.0       | 455    | 1  | US-08-321-668-2    |
| 12         | 941   | 100.0       | 455    | 1  | US-08-837-941-2    |
| 13         | 941   | 100.0       | 455    | 2  | US-08-126-016-2    |
| 14         | 941   | 100.0       | 455    | 2  | US-08-465-982-25   |
| 15         | 941   | 100.0       | 455    | 4  | US-08-815-469-5    |
| 16         | 941   | 100.0       | 455    | 4  | US-09-006-353A-3   |
| 17         | 941   | 100.0       | 455    | 4  | US-09-527-236A-5   |
| 18         | 941   | 100.0       | 455    | 4  | US-08-054-970-2    |
| 19         | 941   | 100.0       | 455    | 4  | US-09-565-918-4    |
| 20         | 941   | 100.0       | 455    | 4  | US-09-573-986-3    |
| 21         | 930.5 | 98.9        | 909    | 4  | US-09-013-895A-4   |
| 22         | 930.5 | 98.9        | 909    | 4  | US-09-448-868-4    |
| 23         | 928   | 98.6        | 285    | 4  | US-08-804-166-6    |
| 24         | 928   | 98.6        | 285    | 4  | US-08-910-991-6    |
| 25         | 925.5 | 98.4        | 453    | 4  | US-09-086-483A-5   |
| 26         | 924   | 98.2        | 199    | 1  | US-08-050-319B-48  |
| 27         | 924   | 98.2        | 199    | 2  | US-08-465-982-48   |

|    |       |      |     |   |                    |                   |
|----|-------|------|-----|---|--------------------|-------------------|
| 28 | 921   | 97.9 | 197 | 4 | US-08-828-683A-21  | Sequence 21, Appl |
| 29 | 904   | 96.1 | 154 | 4 | US-08-828-683A-12  | Sequence 12, Appl |
| 30 | 900   | 95.6 | 133 | 2 | US-08-219-237B-4   | Sequence 4, Appl  |
| 31 | 900   | 95.6 | 133 | 4 | US-08-477-347-12   | Sequence 12, Appl |
| 32 | 900   | 95.6 | 153 | 4 | US-08-476-862-3    | Sequence 3, Appl  |
| 33 | 900   | 95.6 | 153 | 4 | US-08-468-560C-4   | Sequence 4, Appl  |
| 34 | 873   | 92.8 | 154 | 2 | US-08-232-087A-10  | Sequence 10, Appl |
| 35 | 842.5 | 89.5 | 256 | 4 | US-08-804-166-2    | Sequence 2, Appl  |
| 36 | 842.5 | 89.5 | 256 | 4 | US-08-910-991-2    | Sequence 2, Appl  |
| 37 | 837   | 88.9 | 307 | 4 | US-08-804-166-4    | Sequence 4, Appl  |
| 38 | 837   | 88.9 | 307 | 4 | US-08-910-991-4    | Sequence 4, Appl  |
| 39 | 822   | 87.4 | 139 | 4 | US-08-706-945D-129 | Sequence 129, App |
| 40 | 746   | 79.3 | 167 | 1 | US-08-050-319B-2   | Sequence 2, Appl  |
| 41 | 746   | 79.3 | 167 | 1 | US-08-050-319B-57  | Sequence 57, Appl |
| 42 | 746   | 79.3 | 167 | 2 | US-08-465-982-2    | Sequence 2, Appl  |
| 43 | 746   | 79.3 | 167 | 2 | US-08-465-982-57   | Sequence 57, Appl |
| 44 | 731   | 77.7 | 124 | 1 | US-08-050-319B-4   | Sequence 4, Appl  |
| 45 | 731   | 77.7 | 124 | 2 | US-08-465-982-4    | Sequence 4, Appl  |

## ALIGNMENTS

RESULT 1  
US-09-326-394-2  
; Sequence 2, Application US/09326394  
; Patent No. 6306820  
; GENERAL INFORMATION:  
; APPLICANT: Bendele, Alison M.  
; APPLICANT: Sennello, Regina M.  
; APPLICANT: Edwards, Carl K.  
; TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING  
; TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: CA  
; COUNTRY: US  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/326,394  
; FILING DATE: 08-DEC-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/032,587  
; FILING DATE: 06-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,355  
; FILING DATE: 23-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/039,315  
; FILING DATE: 07-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/052,023  
; FILING DATE: 09-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zindrick, Thomas K.  
; REGISTRATION NUMBER: 32,185  
; REFERENCE/DOCKET NUMBER: A-430D  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 161 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-326-394-2

Query Match 100.0%; Score 941; DB 4; Length 161;  
Best Local Similarity 100.0%; Pred. No. 1.6e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGXHYHPONNSICTCKHKGTYLYNDPCPGQDTCRECGSGFTASENHLRHCL 60  
DB 1 DSVCPQGXHYHPONNSICTCKHKGTYLYNDPCPGQDTCRECGSGFTASENHLRHCL 60  
QY 61 SCSKCRKEMQVIEISSCTVDRTVCGCRKNQRYHWSENLFCQCNCSLCNGTVHLSQOE 120  
DB 61 SCSKCRKEMQVIEISSCTVDRTVCGCRKNQRYHWSENLFCQCNCSLCNGTVHLSQOE 120  
QY 121 KONTVCTCHAGFFLRENECVSCSNCKKSLECTKCLPQIEN 161  
DB 121 KONTVCTCHAGFFLRENECVSCSNCKKSLECTKCLPQIEN 161

## RESULT 2

US-08-974-022-46  
Sequence 46, Application US/08974022  
Patent No. 6015938  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ. ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 280 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-022-46

Query Match 100.0%; Score 941; DB 3; Length 280;  
Best Local Similarity 100.0%; Pred. No. 2.7e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGXHYHPONNSICTCKHKGTYLYNDPCPGQDTCRECGSGFTASENHLRHCL 60  
DB 41 DSVCPQGXHYHPONNSICTCKHKGTYLYNDPCPGQDTCRECGSGFTASENHLRHCL 100  
QY 61 SCSKCRKEMQVIEISSCTVDRTVCGCRKNQRYHWSENLFCQCNCSLCNGTVHLSQOE 120  
DB 101 SCSKCRKEMQVIEISSCTVDRTVCGCRKNQRYHWSENLFCQCNCSLCNGTVHLSQOE 160  
QY 121 KONTVCTCHAGFFLRENECVSCSNCKKSLECTKCLPQIEN 161

DB 161 KONTVCTCHAGFFLRENECVSCSNCKKSLECTKCLPQIEN 201

## RESULT 3

US-08-795-445A-46  
Sequence 46, Application US/08795445A  
Patent No. 6284485  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,445A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ. ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 280 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-445A-46

Query Match 100.0%; Score 941; DB 4; Length 280;  
Best Local Similarity 100.0%; Pred. No. 2.7e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGXHYHPONNSICTCKHKGTYLYNDPCPGQDTCRECGSGFTASENHLRHCL 60  
DB 41 DSVCPQGXHYHPONNSICTCKHKGTYLYNDPCPGQDTCRECGSGFTASENHLRHCL 100  
QY 61 SCSKCRKEMQVIEISSCTVDRTVCGCRKNQRYHWSENLFCQCNCSLCNGTVHLSQOE 120  
DB 101 SCSKCRKEMQVIEISSCTVDRTVCGCRKNQRYHWSENLFCQCNCSLCNGTVHLSQOE 160  
QY 121 KONTVCTCHAGFFLRENECVSCSNCKKSLECTKCLPQIEN 161  
DB 161 KONTVCTCHAGFFLRENECVSCSNCKKSLECTKCLPQIEN 201

RESULT 4  
US-08-795-447A-46  
Sequence 46, Application US/08795447A  
Patent No. 6284728  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: Osteoprotegerin

; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: One Amgen Center Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,447A  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378D2  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 280 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-795-447A-46

Query Match 100.0%; Score 941; DB 4; Length 280;  
Best Local Similarity 100.0%; Pred. No. 2.7e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQNNISCTCKCHKGTLYNDGPGQDTCRECESSGFTASENHLRCL 60  
Db 41 DSVCPQGYIHPQNNISCTCKCHKGTLYNDGPGQDTCRECESSGFTASENHLRCL 100  
Qy 61 SCSKCRKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 120  
Db 101 SCSKCRKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 160  
Qy 121 KONTVCTCHAGFFLRENECVSCNCKKSLCTKLCPLQIEN 161  
Db 161 KONTVCTCHAGFFLRENECVSCNCKKSLCTKLCPLQIEN 201

## RESULT 5

US-08-974-186-46  
; Sequence 46, Application US/08974186  
; Patent No. 6284740  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Behavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,186  
; FILING DATE:  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 280 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-974-186-46

Query Match 100.0%; Score 941; DB 4; Length 280;  
Best Local Similarity 100.0%; Pred. No. 2.7e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQNNISCTCKCHKGTLYNDGPGQDTCRECESSGFTASENHLRCL 60  
Db 41 DSVCPQGYIHPQNNISCTCKCHKGTLYNDGPGQDTCRECESSGFTASENHLRCL 100  
Qy 61 SCSKCRKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 120  
Db 101 SCSKCRKEMGOVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 160  
Qy 121 KONTVCTCHAGFFLRENECVSCNCKKSLCTKLCPLQIEN 161  
Db 161 KONTVCTCHAGFFLRENECVSCNCKKSLCTKLCPLQIEN 201

## RESULT 6

US-08-795-446B-46  
; Sequence 46, Application US/08795446B  
; Patent No. 6288032  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Behavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,446B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 280 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-795-446B-46

Query Match 100.0%; Score 941; DB 4; Length 280;  
Best Local Similarity 100.0%; Pred. No. 2.7e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPGKXIHPPNNISICTCKHKGTYLYNDGPGQDTCRCESGSGFTASNNHRLCL 60  
DB 41 DSVCPGKXIHPPNNISICTCKHKGTYLYNDGPGQDTCRCESGSGFTASNNHRLCL 100  
QY 61 SCSKCRKEMQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSOE 120  
DB 101 SCSKCRKEMQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSOE 160  
QY 121 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCUPOIEN 161  
DB 161 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCUPOIEN 201

RESULT 7  
US-08-706-945D-132

/ Sequence 132, Application US/08706945D  
/ Patent No. 6369027  
/ GENERAL INFORMATION:  
/ APPLICANT: Boyle, William  
/ APPLICANT: Lacey, David  
/ APPLICANT: Calzone, Frank  
/ APPLICANT: Chang, Ming-Shi  
/ TITLE OF INVENTION: Osteoprotegerin  
/ FILE REFERENCE: A-378CIP  
/ CURRENT APPLICATION NUMBER: US/08/706,945D  
/ CURRENT FILING DATE: 1996-09-03  
/ PRIOR APPLICATION NUMBER: 08/577,788  
/ PRIOR FILING DATE: 1995-12-22  
/ NUMBER OF SEQ ID NOS: 145  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 132  
/ LENGTH: 280  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-08-706-945D-132

Query Match 100.0%; Score 941; DB 4; Length 280;  
Best Local Similarity 100.0%; Pred. No. 2.7e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPGKXIHPPNNISICTCKHKGTYLYNDGPGQDTCRCESGSGFTASNNHRLCL 60  
DB 41 DSVCPGKXIHPPNNISICTCKHKGTYLYNDGPGQDTCRCESGSGFTASNNHRLCL 100  
QY 61 SCSKCRKEMQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSOE 120  
DB 101 SCSKCRKEMQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSOE 160  
QY 121 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCUPOIEN 161  
DB 161 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCUPOIEN 201

RESULT 8  
US-08-804-166-8

/ Sequence 8, Application US/08804166  
/ Patent No. 6193972  
/ GENERAL INFORMATION:  
/ APPLICANT: Campbell, Robert K.  
/ APPLICANT: Jameson, Bradford A.  
/ APPLICANT: Chappel, Scott C.  
/ TITLE OF INVENTION: HYBRID PROTEINS  
/ NUMBER OF SEQUENCES: 22  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: BROWDY AND NEIMARK  
/ STREET: 419 Seventh Street N.W., Ste. 300  
/ CITY: Washington  
/ STATE: D.C.

/ COUNTRY: USA  
/ ZIP: 22207  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/804,166  
/ FILING DATE:  
/ CLASSIFICATION:  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 60/011,936  
/ FILING DATE: 20 February 1996  
/ CLASSIFICATION:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Browdy, Roger L.  
/ REGISTRATION NUMBER: 25,618  
/ REFERENCE/DOCKET INFORMATION:  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (202) 628-5197  
/ TELEFAX: (202) 737-3528  
/ INFORMATION FOR SEQ ID NO: 8:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 336 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
US-08-804-166-8

Query Match 100.0%; Score 941; DB 4; Length 336;  
Best Local Similarity 100.0%; Pred. No. 3.2e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPGKXIHPPNNISICTCKHKGTYLYNDGPGQDTCRCESGSGFTASNNHRLCL 60  
DB 23 DSVCPGKXIHPPNNISICTCKHKGTYLYNDGPGQDTCRCESGSGFTASNNHRLCL 82  
QY 61 SCSKCRKEMQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSOE 120  
DB 83 SCSKCRKEMQVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSOE 142  
QY 121 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCUPOIEN 161  
DB 143 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCUPOIEN 183

RESULT 9  
US-08-910-991-8

/ Sequence 8, Application US/08910991  
/ Patent No. 6194177  
/ GENERAL INFORMATION:  
/ APPLICANT: Campbell, Robert K.  
/ APPLICANT: Jameson, Bradford A.  
/ APPLICANT: Chappel, Scott C.  
/ TITLE OF INVENTION: HYBRID PROTEINS  
/ NUMBER OF SEQUENCES: 22  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: BROWDY AND NEIMARK  
/ STREET: 419 Seventh Street N.W., Ste. 300  
/ CITY: Washington  
/ STATE: D.C.  
/ COUNTRY: USA  
/ ZIP: 22207  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/910,991  
/ FILING DATE:  
/ CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/804,166  
 FILING DATE: 20 February 1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/011,936  
 FILING DATE: 20 February 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: YUN, Allen C.  
 REGISTRATION NUMBER: 37,971  
 REFERENCE/DOCKET NUMBER: CAMPBELL=2B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 628-5197  
 TELEFAX: (202) 737-3528  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 336 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-910-991-8

Query Match 100.0%; Score 941; DB 4; Length 336;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-76;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQNNISCTCKCHKGTLYLYNDPCPGQDTCRCESGSGFTASENHLRHCL 60  
 Db 23 DSVCPQGYIHPQNNISCTCKCHKGTLYLYNDPCPGQDTCRCESGSGFTASENHLRHCL 82  
 Qy 61 SCSCRKEMGQVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 120  
 Db 83 SCSCRKEMGQVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 142  
 Qy 121 KONTVCTCHAGFFLRENECVSCNCKKSLECTKLCPLQIEN 161  
 Db 143 KONTVCTCHAGFFLRENECVSCNCKKSLECTKLCPLQIEN 183

RESULT 10  
 US-08-050-319B-25  
 Sequence 25, Application US/08050319B  
 Patent No. 5633145  
 GENERAL INFORMATION:  
 APPLICANT: M. Feldmann, P.W. Gray,  
 APPLICANT: M.J.C. Turner, F.M. Brennan  
 TITLE OF INVENTION: Modified human TNFalpha (Tumor  
 Nucleos Factor alpha) Receptor  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Reed & Robbins  
 STREET: 635 Bryant Street  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94301  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/050,319B  
 FILING DATE: 10-May-1993  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Robbins, Roberta L.  
 REGISTRATION NUMBER: 33,208  
 REFERENCE/DOCKET NUMBER: 5150-0030  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 617-8999  
 TELEFAX: (415) 327-3231  
 INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 455 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-050-319B-25

Query Match 100.0%; Score 941; DB 1; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-76;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQNNISCTCKCHKGTLYLYNDPCPGQDTCRCESGSGFTASENHLRHCL 60  
 Db 41 DSVCPQGYIHPQNNISCTCKCHKGTLYLYNDPCPGQDTCRCESGSGFTASENHLRHCL 100  
 Qy 61 SCSCRKEMGQVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 120  
 Db 101 SCSCRKEMGQVEISSCTVDRDTCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 160  
 Qy 121 KONTVCTCHAGFFLRENECVSCNCKKSLECTKLCPLQIEN 161  
 Db 161 KONTVCTCHAGFFLRENECVSCNCKKSLECTKLCPLQIEN 201

RESULT 11  
 US-08-321-668-2  
 Sequence 2, Application US/08321668  
 Patent No. 5658585  
 GENERAL INFORMATION:  
 APPLICANT: WALLACH, David  
 APPLICANT: BRAKEBUSCH, Cord  
 APPLICANT: VARFOLOMEV, Eugene  
 APPLICANT: BATKIN, Michael  
 TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
 TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/321,668  
 FILING DATE: 12-OCT-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: IL 107268  
 FILING DATE: 12-OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: WALLACH=13  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 TELEX: 248633  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 455 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-321-668-2

Query Match 100.0%; Score 941; DB 1; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-76;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPONNSICTCKHKGTYLYNDGPGGDDTTCRCBESSGFTASNNHRLCL 60  
DB 41 DSVCPQGYIHPONNSICTCKHKGTYLYNDGPGGDDTTCRCBESSGFTASNNHRLCL 100  
QY 61 SCSKREKMGQVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSJCLNGTVHLSOE 120  
DB 101 SCSKREKMGQVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSJCLNGTVHLSOE 160  
QY 121 KONTVCTCHAGFFLRENECVCSNCKKSLECTKLCPLPOIEN 161  
DB 161 KONTVCTCHAGFFLRENECVCSNCKKSLECTKLCPLPOIEN 201

RESULT 12  
US-08-837-941-2  
Sequence 2, Application US/08837941  
Patent No. 5766917  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BRAKEBUSCH, Cord  
APPLICANT: VARFOLOMEV, Eugene  
APPLICANT: BATKIN, Michael  
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/837,941  
FILING DATE: 28-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/321,668  
FILING DATE: 12-OCT-1994  
APPLICATION NUMBER: IL 107268  
FILING DATE: 12-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH=13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-837-941-2

Query Match 100.0%; Score 941; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4,3e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPONNSICTCKHKGTYLYNDGPGGDDTTCRCBESSGFTASNNHRLCL 60  
DB 41 DSVCPQGYIHPONNSICTCKHKGTYLYNDGPGGDDTTCRCBESSGFTASNNHRLCL 100  
QY 61 SCSKREKMGQVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSJCLNGTVHLSOE 120  
DB 161 KONTVCTCHAGFFLRENECVCSNCKKSLECTKLCPLPOIEN 201

DB 101 SCSKREKMGQVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSJCLNGTVHLSOE 160  
QY 121 KONTVCTCHAGFFLRENECVCSNCKKSLECTKLCPLPOIEN 161  
DB 161 KONTVCTCHAGFFLRENECVCSNCKKSLECTKLCPLPOIEN 201

RESULT 13  
US-08-126-016-2  
Sequence 2, Application US/08126016  
Patent No. 5811261  
GENERAL INFORMATION:  
APPLICANT: WALLACH, DAVID  
APPLICANT: NOPAR, YARON  
APPLICANT: KEMPER, OLIVER  
APPLICANT: ENGELMANN, HARTMUT  
APPLICANT: BRAKEBUSCH, CORD  
APPLICANT: ADERKA, DAN  
TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR  
TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TNF-1)  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/126,016  
FILING DATE: 24-SEP-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/625668  
FILING DATE: 13-DEC-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, ROGER L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-126-016-2

Query Match 100.0%; Score 941; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4,3e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPONNSICTCKHKGTYLYNDGPGGDDTTCRCBESSGFTASNNHRLCL 60  
DB 41 DSVCPQGYIHPONNSICTCKHKGTYLYNDGPGGDDTTCRCBESSGFTASNNHRLCL 100  
QY 61 SCSKREKMGQVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSJCLNGTVHLSOE 120  
DB 101 SCSKREKMGQVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSJCLNGTVHLSOE 160  
QY 121 KONTVCTCHAGFFLRENECVCSNCKKSLECTKLCPLPOIEN 161  
DB 161 KONTVCTCHAGFFLRENECVCSNCKKSLECTKLCPLPOIEN 201



## RESULT 14

US-08-465-982-25  
; Sequence 25, Application US/08465982  
; Patent No. 5863786  
; GENERAL INFORMATION:  
; APPLICANT: M.Feldmann, P.W. Gray,  
; APPLICANT: M.J.C. Turner, F.M. Brennan  
; TITLE OF INVENTION: Modified human TNFalpha (Tumor  
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reed & Robbins  
; STREET: 635 Bryant Street  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,982  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/050,319  
; FILING DATE: 10-May-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robbins, Roberta L.  
; REGISTRATION NUMBER: 33,208  
; REFERENCE/DOCKET NUMBER: 5150-0030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 617-8999  
; TELEFAX: (415) 327-3231  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-465-982-25

Query Match 100.0%; Score 941; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.3e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRCL 60  
Db 41 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRCL 100

Qy 61 SCSKCRKEMGQVEISSCTVDRDTVCGRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 120  
Db 101 SCSKCRKEMGQVEISSCTVDRDTVCGRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 160

Qy 121 KQNTVCTCHAGFFLRNECVSCSNCKKSLCTKCLPQIEN 161  
Db 161 KQNTVCTCHAGFFLRNECVSCSNCKKSLCTKCLPQIEN 201

Search completed: December 3, 2002, 14:41:46  
Job time : 16 secs

## RESULT 15

US-08-815-469-5  
; Sequence 5, Application US/08815469  
; Patent No. 6153402  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Dillon, Patrick J.  
; TITLE OF INVENTION: Death Domain Containing Receptors  
; NUMBER OF SEQUENCES: 17

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., NW, Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/815,469  
FILING DATE: HEREWITH  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 6153402 Yet Assigned  
FILING DATE: 06-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/028,711  
FILING DATE: 17-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/013,285  
FILING DATE: 12-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-815-469-5

Query Match 100.0%; Score 941; DB 4; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.3e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRCL 60  
Db 41 DSVCPQGYIHPQNNISICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRCL 100

Qy 61 SCSKCRKEMGQVEISSCTVDRDTVCGRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 120  
Db 101 SCSKCRKEMGQVEISSCTVDRDTVCGRKNQYRHYWSENLFQCFNCSCLNGTVHLSQOE 160

Qy 121 KQNTVCTCHAGFFLRNECVSCSNCKKSLCTKCLPQIEN 161  
Db 161 KQNTVCTCHAGFFLRNECVSCSNCKKSLCTKCLPQIEN 201

Search completed: December 3, 2002, 14:41:46  
Job time : 16 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 3, 2002, 14:39:03 ; Search time 17 Seconds  
(without alignments)  
910.450 Million cell updates/sec

Title: US-09-907-263-2

Perfect score: 941

Sequence: 1 DSVCPQGYIHPQNSICT.....CSNCKSECTKLCPLQIEN 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 941   | 100.0       | 455    | 1     | GQHUT1             |
| 2          | 716.5 | 76.1        | 461    | 2     | tumor necrosis fac |
| 3          | 680   | 72.3        | 454    | 1     | tumor necrosis fac |
| 4          | 669   | 71.1        | 461    | 1     | tumor necrosis fac |
| 5          | 187.5 | 19.9        | 435    | 2     | tumor necrosis fac |
| 6          | 182.5 | 19.4        | 427    | 1     | tumor necrosis fac |
| 7          | 181   | 19.2        | 474    | 2     | nerve growth facto |
| 8          | 179.5 | 19.1        | 326    | 1     | tumor necrosis fac |
| 9          | 178   | 18.9        | 325    | 2     | T2 protein - myxom |
| 10         | 176.5 | 18.8        | 425    | 1     | T2 protein - rabbi |
| 11         | 176   | 18.7        | 459    | 2     | nerve growth facto |
| 12         | 167.5 | 17.8        | 305    | 2     | Gene murine tumour |
| 13         | 166.5 | 17.7        | 349    | 2     | B cell-associated  |
| 14         | 164   | 17.4        | 348    | 2     | G2R protein - vari |
| 15         | 164   | 17.4        | 349    | 2     | hypothetical prote |
| 16         | 162.5 | 17.3        | 327    | 2     | gene G4R protein   |
| 17         | 161   | 17.1        | 461    | 1     | apoptosis-mediati  |
| 18         | 158.5 | 16.8        | 651    | 2     | tumor necrosis fac |
| 19         | 147.5 | 15.7        | 677    | 2     | death receptor-6   |
| 20         | 147   | 15.6        | 324    | 2     | trophozoite cystei |
| 21         | 145   | 15.4        | 416    | 1     | Fas antigen precu  |
| 22         | 141   | 15.0        | 1680   | 2     | nerve growth facto |
| 23         | 139.5 | 14.8        | 250    | 1     | furin EC 3.4.21.7  |
| 24         | 139.5 | 14.8        | 260    | 1     | CD27 antigen precu |
| 25         | 139.5 | 14.8        | 277    | 2     | CD27 antigen precu |
| 26         | 134   | 14.2        | 1548   | 2     | B-cell activation  |
| 27         | 132   | 14.0        | 899    | 2     | serine proteinase  |
| 28         | 132   | 14.0        | 915    | 2     | subtilisin-like pr |
| 29         | 131.5 | 14.0        | 272    | 2     | subtilisin-like pr |
|            |       |             |        |       | gene ox40 protein  |

## ALIGNMENTS

### RESULT 1

GQHUT1

tumor necrosis factor receptor 1 precursor [validated] - human

N;Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1

C;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text change 08-Dec-2000

C;Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A38:

R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.

Genomics 13, 219-224, 1992

A;Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to chi

A;Reference number: A38208; MUID:92250049; PMID:1315717

A;Accession: A38208

A;Molecule type: DNA

A;Residues: 1-455 <FUC>

A;Cross-references: GB:M75865; GB:M75864; GB:M75866; NID:G339748; PIDN:AAA61201.1; PID:G:

R;Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslau

Cell 61, 351-359, 1990

A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recept

A;Reference number: A34899; MUID:90235284; PMID:2158862

A;Accession: A34899

A;Molecule type: mRNA

A;Residues: 1-455 <LOS>

A;Cross-references: GB:M58286; GB:M33480; NID:G339753; PIDN:AAA36753.1; PID:G339754

A;Experimental source: placenta

A;Note: part of this sequence, including the amino end of the mature protein, confirmed i

R;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.;

Cell 61, 361-370, 1990

A;Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.

A;Reference number: A34900; MUID:90235285; PMID:2158863

A;Accession: A34900

A;Molecule type: mRNA

A;Residues: 1-455 <SCH>

A;Cross-references: GB:M33294; NID:G339744; PIDN:AAA03210.1; PID:G339745

R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; C

DNA Cell Biol. 9, 705-715, 1990

A;Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto

A;Reference number: A36555; MUID:91090841; PMID:1702293

A;Accession: A36555

A;Molecule type: mRNA

A;Residues: 1-455 <HIM>

A;Cross-references: GB:M63121; NID:G339755; PIDN:AAA36754.1; PID:G339756

A;Accession: C36555

A;Molecule type: protein

A;Residues: 30-38;41-53, 'X', '55-79, 'XX', '82-94, 'NK', '100-104;107-128;162-167, 'X', '169-20

A;Note: the purified protein, called tumor necrosis factor binding protein, is a soluble

R;Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.

Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990

A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of rec

A;Reference number: A38281; MUID:91017509; PMID:2170974

A;Accession: A38281

A;Molecule type: mRNA

A:Residues: 1-455 <GRA>  
 A:Cross-references: GB:M37764  
 A:Note: The authors translated the codon TCG for residue 371 as Thr, AAG for residue 372  
 R:Kempner, Y.; Kempner, O.; Brakheusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann  
 EMO J. 9, 3269-3278, 1990  
 A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type  
 1 form of the receptor.  
 A:Reference number: S12057; MUID:91006021; PMID:1698610  
 A:Accession: S12057  
 A:Molecule type: mRNA  
 A:Residues: 1-455 <NOP>  
 A:Cross-references: EMBL:X55313; NID:g37223; PIDD:CA39021.1; PID:g37224  
 A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w  
 R:Kempner, O.; Wallach, D.  
 Gene 134, 209-216, 1993  
 A:Title: Cloning and partial characterization of the promoter for the human p55 tumor ne  
 A:Reference number: J70758; MUID:94085779; PMID:8262379  
 A:Accession: J70758  
 A:Molecule type: DNA  
 A:Residues: 1-13 <KEM>  
 R:Secklinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
 Eur. J. Immunol. 20, 1167-1174, 1990  
 A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc  
 A:Reference number: A60231; MUID:90292116; PMID:2113477  
 A:Accession: A60231  
 A:Molecule type: protein  
 A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>  
 R:Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucchi III, J.A.; Jeffes, E.W.B.; Le  
 Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
 A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto  
 clients.  
 A:Reference number: A38258; MUID:91062364; PMID:2174164  
 A:Accession: A38258  
 A:Molecule type: protein  
 A:Residues: 41-60 <GAT>  
 A:Experimental source: cancer patient serum  
 R:Olsson, I.; Lantiz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.  
 Eur. J. Haematol. 42, 270-275, 1999  
 A:Title: Isolation and characterization of a tumor necrosis factor binding protein from  
 A:Reference number: A60594; MUID:89171156; PMID:2924890  
 A:Accession: A60594  
 A:Molecule type: protein  
 A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'X', 60 <OLS>  
 A:Experimental source: renal failure patient urine  
 R:Engelmann, H.; Novick, D.; Wallach, D.  
 J. Biol. Chem. 265, 1531-1536, 1990  
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
 A:Reference number: A35010; MUID:90110215; PMID:2153136  
 A:Accession: A35010  
 A:Molecule type: protein  
 A:Residues: 41-45 <ENG>  
 A:Experimental source: normal urine  
 R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.  
 Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994  
 A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f  
 A:Reference number: JC2404; MUID:9518033; PMID:7765720  
 A:Accession: JC2404  
 A:Molecule type: protein  
 A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KXJ>  
 A:Experimental source: urine  
 C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
 C:Genetics:  
 A:Gene: GDB:TNFR1  
 A:Cross-references: GDB:125913; OMIM:191190  
 A:Map position: 12p13.2-12p13.2  
 A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-45/Product: tumor necrosis factor receptor 1 #status predicted <MAT>  
 F:30-211/Domain: extracellular #status predicted <EXT>  
 F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
 F:44-82/Domain: NGF receptor repeat homology <NG1>

F:84-126/Domain: NGF receptor repeat homology <NG2>  
 F:127-167/Domain: NGF receptor repeat homology <NG3>  
 F:168-196/Domain: NGF receptor repeat homology <NG4>  
 F:212-234/Domain: transmembrane #status predicted <MEM>  
 F:235-455/Domain: intracellular #status predicted <INT>  
 F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 941; DB 1; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 8,3e-62;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQKGIHPNNNSICCTKCHKGTLYNDPCPGQDPTDCRECSGSFTASENHLRHCL 60  
 DB 41 DSVCPQKGIHPNNNSICCTKCHKGTLYNDPCPGQDPTDCRECSGSFTASENHLRHCL 100

QY 61 SCSKCKEMGVEISCTVDRTVCGCRKNQYRHWSENLFOCFNCSCLINGTVHLSQCE 120  
 DB 101 SCSKCKEMGVEISCTVDRTVCGCRKNQYRHWSENLFOCFNCSCLINGTVHLSQCE 160

QY 121 KONTVCTCHAGFPLRENECVSCNCKSLBECTKCLPOIEN 161  
 DB 161 KONTVCTCHAGFPLRENECVSCNCKSLBECTKCLPOIEN 201

RESULT 2  
 JC4302  
 tumor necrosis factor receptor p55 precursor - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Jul-1999  
 C:Accession: JC4302; PC4093  
 R:Stuer, B.; Paul, U.  
 Gene 163, 263-266, 1995  
 A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.  
 A:Reference number: JC4302; MUID:96011645; PMID:7590278  
 A:Accession: JC4302  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <SUT>  
 A:Cross-references: GB:U19994; NID:g1141752; PIDD:AAC48499.1; PID:g1141753  
 A:Accession: PC4093  
 A:Molecule type: protein  
 A:Residues: 1-7 <SUT>  
 A:Experimental source: kidney cell line 15  
 C:Genetics:  
 A:Gene: tnfr  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>  
 F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>  
 F:44-82/Domain: NGF receptor repeat homology <NG1>  
 F:84-126/Domain: NGF receptor repeat homology <NGF>  
 F:211-231/Domain: transmembrane #status predicted <TM>  
 F:361-447/Domain: signal transduction #status predicted <SIT>  
 F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.1%; Score 716.5; DB 2; Length 461;  
 Best Local Similarity 77.4%; Pred. No. 2e-45;  
 Matches 120; Conservative 12; Mismatches 22; Indels 1; Gaps 1;

QY 1 DSVCPQKGIHPNNNSICCTKCHKGTLYNDPCPGQDPTDCRECSGSFTASENHLRHCL 60  
 DB 41 DSVCPQKGIHPNNNSICCTKCHKGTLYNDPCPGQDPTDCRECSGSFTASENHLRHCL 100

QY 61 SCSKCKEMGVEISCTVDRTVCGCRKNQYRHWSENLFOCFNCSCLINGTVHLSQCE 120  
 DB 101 SCSKCKEMGVEISCTVDRTVCGCRKNQYRHWSENLFOCFNCSCLINGTVHLSQCE 160

QY 121 KONTVCTCHAGFPLRENECVSCNCKSLBECTKCL 155  
 DB 161 KONTVCTCHAGFPLRENECVSCNCKSLBECTKCL 194

RESULT 3

## GOMSTI

tumor necrosis factor receptor 1 precursor - mouse  
N:Alternate names: tumor necrosis factor receptor, 55K  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 01-Dec-2000  
C:Accession: A38634; B40254; S16677; S19021; I54532; I57826  
R:Lewis, M.; Tartaglin, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.  
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor  
A:Reference number: A38634; MUID:91187885; PMID:1849278  
A:Accession: A38634  
A:Molecule type: mRNA  
A:Residues: 1-454 <LEW>  
R:Cross-references: GB:M60468; NID:G199825; PIDN:AAA39751.1; PID:G199826  
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk  
Mol. Cell. Biol. 11, 3020-3026, 1991  
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for  
A:Reference number: A40254; MUID:91246168; PMID:1645445  
A:Accession: B40254  
A:Molecule type: mRNA  
A:Residues: 1-454 <GO2>  
R:Cross-references: GB:M60468; NID:G199825; PIDN:AAA39751.1; PID:G199826  
R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissnerghis, A.M.; Gray, P.W.; Feldma  
Eur. J. Immunol. 21, 1645-1656, 1991  
A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis  
A:Reference number: S16677; MUID:91285014; PMID:1647956  
A:Accession: S16677  
A:Molecule type: mRNA  
A:Residues: 1-454 <BAR>  
R:Cross-references: EMBL:X59238; NID:G53578; PIDN:CAA41922.1; PID:G53579  
R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.  
Immunogenetics 34, 338-340, 1991  
A:Title: Molecular cloning and expression of the mouse Tnf receptor type b.  
A:Reference number: S19021; MUID:92039815; PMID:1657766  
A:Accession: S19021  
A:Molecule type: mRNA  
A:Residues: 1-454 <ROT>  
R:Cross-references: EMBL:X57796; NID:G54848; PIDN:CAA40936.1; PID:G54849  
R:Bebo, B.F.  
Immunogenetics 39, 450-451, 1994  
A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell  
A:Reference number: I54532; MUID:94245292; PMID:8188324  
A:Accession: I54532  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-454 <RES>  
R:Cross-references: GB:L26349; NID:G430732; PIDN:AAA59361.1; PID:G430733  
R:Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.  
Mol. Immunol. 30, 165-176, 1993  
A:Title: Genomic organization and promoter function of the murine tumor necrosis factor  
A:Reference number: I57826; MUID:93156721; PMID:8381516  
A:Accession: I57826  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-393 'G', 395-454 <RE2>  
R:Cross-references: GB:W76656; NID:G202100; PIDN:AAA0465.1; PID:G202102  
C:Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca  
C:Genetics:  
A:Gene: TNFR-2  
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C:Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protei  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
F:30-212/Domain: extracellular #status predicted <EXT>  
F:44-82/Domain: NGF receptor repeat homology <NG1>  
F:84-126/Domain: NGF receptor repeat homology <NG2>  
F:127-167/Domain: NGF receptor repeat homology <NG3>  
F:168-204/Domain: NGF receptor repeat homology <NG4>  
F:213-235/Domain: transmembrane #status predicted <MEM>  
F:236-454/Domain: intracellular #status predicted <INT>  
F:54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.3%; Score 680; DB 1; Length 454;  
Best Local Similarity 71.3%; Pred. No. 9,1e-43;  
Matches 112; Conservative 19; Mismatches 26; Indels 0; Gaps 0;  
QY 1 DSVCPQGYIHPONNSICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRHLCL 60  
Db 41 DSLCPQGYVHSHKNNNSICTCKHKGTYLYVSDCPSPGPDIVCRECKGTFTASQNYLRQCL 100  
QY 61 SCSCKRKEWGQVEISSCTVDRDTCGCRKNQYRHYWSENLFCQFNCSCLNGTVHLSQOE 120  
Db 101 SKCTCRKEMFQVEISPCQADKDTVCCKENQFQYLSLSTHFQCVDCSPCFNGTWTIPCKE 160  
QY 121 KONTVCTCHAGFFLRENECVSCNCKKSLCTKLCPLP 157  
Db 161 TQNTVCNCHAGFFLRESECVFSCCKNECKMLCLP 197

## RESULT 4

## GORTT1

tumor necrosis factor receptor 1 precursor - rat  
N:Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1992 #sequence\_revision 07-Oct-1994 #text\_change 22-Jun-1999  
C:Accession: B36555  
R:Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;  
DNA Cell Biol. 9, 705-715, 1990  
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor  
A:Reference number: A36555; MUID:91090841; PMID:1702293  
A:Accession: B36555  
A:Molecule type: mRNA  
A:Residues: 1-461 <HIM>  
R:Cross-references: GB:M63122; NID:G207361; PIDN:AAA42256.1; PID:G207362  
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
F:30-211/Domain: extracellular #status predicted <EXT>  
F:44-82/Domain: NGF receptor repeat homology <NG1>  
F:84-126/Domain: NGF receptor repeat homology <NG2>  
F:127-167/Domain: NGF receptor repeat homology <NG3>  
F:168-204/Domain: NGF receptor repeat homology <NG4>  
F:212-234/Domain: transmembrane #status predicted <MEM>  
F:235-461/Domain: intracellular #status predicted <INT>  
F:54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 71.1%; Score 669; DB 1; Length 461;  
Best Local Similarity 68.3%; Pred. No. 5.8e-42;  
Matches 110; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPONNSICTCKHKGTYLYNDPCPGQDTCRECSGSFTASENHLRHLCL 60  
Db 41 DNLCPQGYIHPONNSICTCKHKGTYLYVSDCPSPGQDTCRECKGTFTASQNHVRQCL 100  
QY 61 SCSCKRKEWGQVEISSCTVDRDTCGCRKNQYRHYWSENLFCQFNCSCLNGTVHLSQOE 120  
Db 101 SKCTCRKEMFQVEISPCQADKDTVCCKENQFQYLSLSTHFQCVDCSPCFNGTWTIPCKE 160  
QY 121 KONTVCTCHAGFFLRENECVSCNCKKSLCTKLCPLP 161  
Db 161 KONTVCNCHAGFFLSGNECTPCSHCKKQNECKMLCLPPVAN 201

## RESULT 5

## I34182

tumor necrosis factor receptor 2-related protein - human  
C:Species: Homo sapiens (man)  
C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000  
C:Accession: I34182  
R:Baens, M.; Chafanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.  
Genomics 16, 214-218, 1993  
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequenc

A:Reference number: 154182; MUID:93252381; PMID:8486360  
 A:Accession: 154182  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-435 <RES>  
 A:Cross-references: GB:L04270; NID:9339761; PIDN:AAA36757.1; PID:9339762  
 A:Genetics:  
 A:Gene: GDB:LTBR  
 A:Cross-references: GDB:1230195; OMIM:600979  
 A:Map position: 12p13.3-12p13.1  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 19.9%; Score 187.5; DB 2; Length 435;  
 Best Local Similarity 32.7%; Pred. No. 7.4e-07;  
 Matches 49; Conservative 17; Mismatches 71; Indels 13; Gaps 7;

QY 8 KYIHPONNISICTCKHKGTYLYNDPCPGQDTCCRECSFASBNHLRHCLSCSKCRK 67  
 Db 49 EYVEPQHR-ICCSRCPPGTIVASAKC-SRIRDTCATCAENSYHNMVLTTCOLCRPCDP 106  
 QY 68 EMGOVEISSCTVDPDTCVCGCRKNQYRHVSENLFOCFNCSL--CLNGTVHLSQCE--KQ 122  
 Db 107 VMGLEEIPAPCTSKRKXTCRCQCPGMFCAANA---LECHTCELLSDCPGCTEALKDEVGKG 163

QY 123 NTVCT-CHAGFLURENECVSCNCKSLK 151  
 Db 164 NNHCVPCKAGHF--QNTSSPASCQPHTRC 191

RESULT 6  
 GQHUN  
 nerve growth factor receptor precursor, low affinity [validated] - human  
 N:Alternate names: NGF receptor  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text\_change 08-Dec-2000  
 C:Accession: A25218; A60204; S21689; I57638  
 R:Johnson, D.; Lanahan, A.; Buck, C.R.; Segal, A.; Morgan, C.; Mercer, E.; Bothwell, M.  
 Cell 47, 545-554, 1986  
 A:Title: Expression and structure of the human NGF receptor.  
 A:Reference number: A25218; MUID:87051725; PMID:3022937  
 A:Accession: A25218  
 A:Molecule type: mRNA  
 A:Residues: 1-427 <UOH>  
 A:Cross-references: GB:M14764; NID:9189204; PIDN:AA59544.1; PID:9189205  
 R:Marano, N.; Diezschold, B.; Farley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.;  
 J. Neurochem. 48, 225-232, 1987  
 A:Title: Purification and amino terminal sequencing of human melanoma nerve growth factor  
 A:Reference number: A60204; MUID:87085574; PMID:3025363  
 A:Accession: A60204  
 A:Molecule type: protein  
 A:Residues: 29-31, 'T', '33-42', 'TT', '45-46', 'TX', '50-51', 'XX', '54-56' <MAR>  
 A:Experimental source: melanoma cell line A875  
 A:Note: This sequence has been corrected by a note added in proof to follow the nucleot  
 R:Vissavajhala, P.; Leszyk, J.D.; Lih-Goetke, J.; Ross, A.H.  
 Arch. Biochem. Biophys. 294, 244-252, 1992  
 A:Title: Structural domains of the extracellular domain of human nerve growth factor rec  
 A:Reference number: S21689; MUID:92198017; PMID:1372422  
 A:Accession: S21689  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 185-208 <VIS>  
 R:Sengal, A.; Patil, N.; Chao, M.  
 Mol. Cell. Biol. 8, 3160-3167, 1988  
 A:Title: A constitutive promoter directs expression of the nerve growth factor receptor  
 A:Reference number: I57638; MUID:89096903; PMID:2850481  
 A:Accession: I57638  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-22 <RES>  
 A:Cross-references: GB:M21621; NID:9189206; PIDN:AAA36363.1; PID:9189207  
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c  
 C:Comment: The cytosolic-rich region of the extracellular domain may form part or all of  
 C:Comment: This protein is thought to form a high-affinity receptor when it associates w

C:Comment: This receptor undergoes both N- and O-linked glycosylation.  
 C:Genetics:  
 A:Gene: GDB:NGFR  
 A:Cross-references: GDB:120234; OMIM:162010  
 A:Map position: 17q21-17q22  
 C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;  
 F:1-28/Domain: signal sequence #status predicted <Sig>  
 F:19-248/Region: extracellular #status predicted <EXT>  
 F:29-250/Domain: extracellular #status predicted <EXT>  
 F:32-65/Domain: NGF receptor repeat homology <NG1>  
 F:67-106/Domain: NGF receptor repeat homology <NG2>  
 F:109-147/Domain: NGF receptor repeat homology <NG3>  
 F:149-189/Domain: NGF receptor repeat homology <NG4>  
 F:197-248/Region: serine/threonine-rich  
 F:251-272/Domain: transmembrane #status predicted <TRM>  
 F:273-427/Domain: intracellular #status predicted <INT>  
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 182.5; DB 1; Length 427;  
 Best Local Similarity 32.4%; Pred. No. 1.7e-06;  
 Matches 52; Conservative 25; Mismatches 62; Indels 23; Gaps 11;

QY 4 CPQGYIHPONNISICTCKHKGTYLYNDPCPGQDTCCRECSFASBNHLRHCLSC 62  
 Db 32 CPTGLYTH---SGECACACNLGEGVAQPC-GANO-TYCEFLDSVTSTDVASATEPCKPC 86

QY 63 SKCRKEMGOVEISS-CTVDRDTCVCGCRKNQYRHVSENLFOCFNCSLCLNGT-VHLSQCE 120  
 Db 87 TEC---VQLQSMASAPCVADAVACRC---AVGYQDETGTGRCACRVCAGSGLVFSCOD 140

QY 121 KQNTVC-TCHAGFLURE---NECVSCSNC---KSLLECKR 153  
 Db 141 KQNTVCCECPDGTYSDEANHVDPCLPCTVCEDTERTQLRECTR 182

RESULT 7  
 B38634  
 tumor necrosis factor receptor type 2 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text\_change 23-Jul-1999  
 C:Accession: B38634; A40254; S54816  
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E  
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor  
 A:Reference number: A38634; MUID:91187885; PMID:1849278  
 A:Accession: B38634  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <LEW>  
 A:Cross-references: GB:M60469; NID:9199827; PIDN:AAA39752.1; PID:9199828  
 R:Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jen  
 Mol. Cell. Biol. 11, 3020-3026, 1991  
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for  
 A:Reference number: A40254; MUID:91246168; PMID:1645445  
 A:Accession: A40254  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <GOO>  
 A:Cross-references: GB:M60469; NID:9199827; PIDN:AAA39752.1; PID:9199828  
 R:Kisilevsky, M.; Fellous, R.; Feldmann, M.; Chernogovskiy, Y.  
 submitted to the EMBL Data Library, May 1995  
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor.  
 A:Reference number: S54816  
 A:Accession: S54816  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-22 <KIS>  
 A:Cross-references: EMBL:X87128; NID:9809043; PIDN:CAA60618.1; PID:9809044  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 C:Keywords: cytokine receptor; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <Sig>  
 F:23-474/Region: extracellular #status predicted <EXT>  
 F:40-77/Domain: NGF receptor repeat homology <NG1>  
 F:79-120/Domain: NGF receptor repeat homology <NG2>

F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 19.2%; Score 181; DB 2; Length 474;  
Best Local Similarity 31.7%; Pred. No. 2.3e-06;  
Matches 51; Conservative 20; Mismatches 76; Indels 14; Gaps 8;

QY 4 CPQGVYIHQNNISICTCKHGTLYNDGPGQDTRCECSGFTASENHLRHLCLSC- 62  
Db 40 CQTSQBYDRKQACAKCPGQYVXHF- NKTSDTVACDEASMTQVWQFRICLSCS 98  
QY 63 SKCRKEMGOVEISSCTVDRTVCGCRKNQY----RHYWSENLPQCFNCSLCLNG-TVHLS 117  
Db 99 SCSCTTD-QVEIRACTQQRNVACBAGRYCALKTH--SGSCRCQWRUSKCPGPGFVASS 154  
QY 118 COBKONTVC-TCHAGPFLRENECVSCNCKSLECKLCLP 157  
Db 155 RAPNGNVLCACAPGTF--SDTTSSTDVCRPHRICSLAIP 193

RESULT 8  
GQVZML

T2 protein - myxoma virus (strain Lausanne)  
C:Species: myxoma virus  
C:Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 18-Jun-1999  
C:Accession: A40566  
R:Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.  
Virology 184, 370-382, 1991  
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor  
A:Reference number: A40566; MUID:91335768; PMID:1651597  
A:Accession: A40566  
A:Molecule type: DNA  
A:Residues: 1-326 <UPT>  
A:Cross-references: GB:M95181; GB:M37976; NID:G332309; PIDN:AAA46632.1; PID:G332310  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
C:Keywords: glycoprotein  
F:64-105/Domain: NGF receptor repeat homology <NG2>  
F:106-147/Domain: NGF receptor repeat homology <NG3>  
F:166.181.205.238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.1%; Score 179.5; DB 1; Length 326;  
Best Local Similarity 27.4%; Pred. No. 2.3e-06;  
Matches 51; Conservative 19; Mismatches 67; Indels 49; Gaps 7;

QY 13 QNNSICTCKHGTLYNDGPGQDTRCECSGFTASENHLRHLCLSC-SKCRKEMGO 71  
Db 34 EKDGJCTSCPPGYSASRLC-GPGSDTVCSPCNKTFTASTNHAPACVSCRCRGTGHL- 91

QY 72 VEISSCTVDRTVCGCRKNQY-----SLECKLCLP 157  
Db 92 -ESQSCDTRDRVCDGAGNYLLKGQGCRCAPKTKCPAGYGVSGHTRTGDVLTCKP 150

QY 93 RHYWSENLPQCFNCSLCLNG-TVHLSCOEKONTVCTCHAGPFLRENECVSCNCKKSLEC 151  
Db 151 RYTYDAVSSTETCTSSFNYSVFNLPVNDTSCTTTAG----PNEVVKTSFESVTLNH 206

QY 152 TKLCLP 157  
Db 207 TD-CDP 211

RESULT 9  
B43692

T2 protein - rabbit fibroma virus  
C:Species: rabbit fibroma virus, Shope fibroma virus  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: B43692  
R:Upton, C.; DeLange, A.M.; Mcfadden, G.  
Virology 160, 20-30, 1987  
A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric  
A:Reference number: A43692; MUID:87321103; PMID:2820128  
A:Accession: B43692  
A>Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-325 <UPT>

A:Cross-references: GB:M17433  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
F:64-105/Domain: NGF receptor repeat homology <NG2>  
F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 18.9%; Score 178; DB 2; Length 325;  
Best Local Similarity 29.6%; Pred. No. 3e-06;  
Matches 45; Conservative 15; Mismatches 62; Indels 30; Gaps 6;

QY 13 QNNSICTCKHGTLYNDGPGQDTRCECSGFTASENHLRHLCLSC-SKCRKEMGO 71  
Db 34 EKDGLCCASCHPGFYASRLC-GPGSNTVCSPCEDGFTASTNHAPACVSCRCRGTGHL- 91

QY 72 VEISSCTVDRTVCGCRKNQYRHYWSENLPQCFNCSLCLNGTVHLSCOEKONTVCTCHAG 131  
Db 92 -ESQPCDTRDRVCDGAGNYLLKGQ-----GCRICAPQT-----KCPAG 132

QY 132 PFLRENECVSCNCKK-----SLECKLCLP 155

Db 133 YGVSGHTRAGDTLCEKCPHPTYSDSLSPTERC 164

RESULT 10  
A26431

Nerve growth factor receptor precursor, low affinity - rat  
N:Alternate names: NGF receptor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A26431; PH1229  
R:Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.  
Nature 325, 593-597, 1987  
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.  
A:Reference number: A26431; MUID:87115859; PMID:3027580  
A:Accession: A26431  
A:Molecule type: mRNA  
A:Residues: 1-425 <RAD>  
A:Cross-references: GB:X05137; NID:G56755; PIDN:CAA28783.1; PID:G56756  
R:Metz, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.  
Gene 121, 247-254, 1992  
A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoic

Query Match 19.1%; Score 179.5; DB 1; Length 326;  
Best Local Similarity 27.4%; Pred. No. 2.3e-06;  
Matches 51; Conservative 19; Mismatches 67; Indels 49; Gaps 7;

QY 13 QNNSICTCKHGTLYNDGPGQDTRCECSGFTASENHLRHLCLSC-SKCRKEMGO 71  
Db 34 EKDGJCTSCPPGYSASRLC-GPGSDTVCSPCNKTFTASTNHAPACVSCRCRGTGHL- 91

QY 72 VEISSCTVDRTVCGCRKNQY-----SLECKLCLP 157  
Db 92 -ESQSCDTRDRVCDGAGNYLLKGQGCRCAPKTKCPAGYGVSGHTRTGDVLTCKP 150

QY 93 RHYWSENLPQCFNCSLCLNG-TVHLSCOEKONTVCTCHAGPFLRENECVSCNCKKSLEC 151  
Db 151 RYTYDAVSSTETCTSSFNYSVFNLPVNDTSCTTTAG----PNEVVKTSFESVTLNH 206

QY 152 TKLCLP 157  
Db 207 TD-CDP 211

RESULT 9  
B43692

T2 protein - rabbit fibroma virus  
C:Species: rabbit fibroma virus, Shope fibroma virus  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: B43692  
R:Upton, C.; DeLange, A.M.; Mcfadden, G.  
Virology 160, 20-30, 1987  
A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric  
A:Reference number: A43692; MUID:87321103; PMID:2820128  
A:Accession: B43692  
A>Status: preliminary  
A:Molecule type: DNA

Query Match

Best Local Similarity 18.8%; Score 176.5; DB 1; Length 425;  
Matches 50; Conservative 25; Mismatches 68; Indels 19; Gaps 10;

QY 4 CPQGVYIHQNNISICTCKHGTLYNDGPGQDTRCECSGFTASENHLRHLCLSC 62  
Db 33 CSTGLYTH---SGECCKACNLGEGVAQPC-GANQ-TVCEPLDNVTFSDVVSATEPCPKPC 87

QY 63 SKCRKMGQVEISS-CTVDRDTVCGCRKQYRHVWSENLFQCFNCSLCLNGT-VHLSQGE 120  
 Db 88 TEC---LGQSMAPCEVEDDANCR---AYGYODEBEGHCEAGVCVSGLVFSCOD 141  
 QY 121 KONTVC-TCHAGFLRE---NECVSCSNCKSLECTKLCPLP 157  
 Db 142 KONTVCCECEPGETYSDANHVDPCLPCTVCEDETEROLRECTP 183  
 RESULT 11  
 148854  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999  
 C/Accession: 148854  
 R/Powell, E.E.; Micker, L.S.; Peterson, L.B.; Todd, J.A.  
 Mamm. Genome 5, 726-727, 1994  
 A>Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
 A/Reference number: 148854; MUID:95178848; PMID:7873884  
 A/Accession: 148854  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-458 <RES>  
 A/Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831  
 C/Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 F:151-188/Domain: NGF receptor repeat homology <NGF>  
 Query Match 18.7%; Score 176; DB 2; Length 459;  
 Best Local Similarity 31.1%; Pred. No. 5, 3e-06;  
 Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;  
 QY 4 CPQGYIHPQNNISICTCKHKGTYLYNDCPGQDTPDCECESSGFTASENHLRHCLSC 62  
 Db 25 CQISQEVYDKAKQCKAKCPGQVVKFC-NKTSDFVACDCEASMYTQVNNPRTCLSCS 83  
 QY 63 SKCRKMGQVEISSCTVDRDTVCGCRKQYRHVWSENLFQCFNCSLCLNGT-VHLS 117  
 Db 84 SSCSTD--QVETRACTQQRNVCACEAGRYCALKTH--SGSCQCKRLSKCPGFGVASS 139  
 QY 118 COEKONTVC-TCHAGFLRENECVSCNCKSLECTKLCPLP 157  
 Db 140 RANGNVLCRAKAPGTF--SPTTSTDVCRPHRISLALP 178  
 RESULT 12  
 A46476  
 C:Species: Mus musculus (house mouse)  
 C>Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Nov-2000  
 C/Accession: A46476; A46515  
 R/Torres, R.M.; Clark, E.A.  
 J. Immunol. 148, 620-626, 1992  
 A>Title: Differential increase of an alternatively polyadenylated mRNA species of murine  
 A/Reference number: A46476; MUID:92105763; PMID:11370315  
 A/Accession: A46476  
 A>Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-305 <TOR>  
 A/Cross-references: GB:M83312; NID:g1553058  
 A/Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)  
 R/Note: this translation is not annotated in GenBank entry M83312, release 113.0  
 R/Gimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,  
 J. Immunol. 149, 3921-3926, 1992  
 A>Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
 A/Reference number: A46515; MUID:93094586; PMID:1281194  
 A/Accession: A46515  
 A>Status: preliminary; not compared with conceptual translation  
 A/Molecule type: nucleic acid  
 A/Residues: 1-287, 'LV' <GRI>  
 A/Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; N  
 A/Experimental source: BALB/C, liver  
 A/Note: sequence extracted from NCBI backbone (NCBI:P:120357)  
 C/Comment: For an alternative splice form, see PIR:A46515.

C/Comment: For an alternative splice form, see PIR:A46476.  
 C/Superfamily: CD27 antigen; NGF receptor repeat homology  
 C/Keywords: alternative splicing; transmembrane protein  
 F:105-144/Domain: NGF receptor repeat homology <NGF>  
 Query Match 17.8%; Score 167.5; DB 2; Length 305;  
 Best Local Similarity 29.9%; Pred. No. 1, 7e-05;  
 Matches 46; Conservative 23; Mismatches 72; Indels 13; Gaps 7;  
 QY 4 CPQGYIHPQNNISICTCKHKGTYLYNDCPGQDTPDCECESSGFTASENHLRHCLSCS 63  
 Db 26 CSDQYIHL---DQCQCDLCPGSRITSHCTAL-EXTQCHPCDSGFSQAQWNRIRCHQR 81  
 QY 64 KCRKMGQVEISSCTVDRDTVCGCRKQYRHVWSENLFQCFNCSLCLNGT-VHLSQGEKQ 122  
 Db 82 HCEBNQIGRVKKEGTASTDVTCTCKEQ--HCTSKCEACQHTPCIPGFGVEMATEFTT 139  
 QY 123 NTVC-TCHAGFLREN---ECVSCSNCK-KSLE 150  
 Db 140 DTVCHPCVGFVFSQSSLFKCYMTWCEDKNLE 173  
 RESULT 13  
 D72175  
 C2R protein - variola minor virus (strain Garcia-1966)  
 C/Species: variola minor virus  
 C/Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 20-Jun-2000  
 C/Accession: D72175  
 R/Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safironov, P.F.; Massung, R.F.; Lopat  
 submitted to GenBank, March 1998  
 A>Description: Analysis of the complete coding sequence of DNA of alacstim variola mino  
 A/Reference number: A72150  
 A/Accession: D72175  
 A>Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-349 <SHC>  
 A/Cross-references: GB:Y16780; NID:95830555; PIDN:CAB54798.1; PID:95830759  
 A/Experimental source: strain Garcia-1966  
 A/Genetics:  
 A/Gene: G2R  
 C/Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
 Query Match 17.7%; Score 166.5; DB 2; Length 349;  
 Best Local Similarity 26.7%; Pred. No. 2, 2e-05;  
 Matches 46; Conservative 19; Mismatches 64; Indels 43; Gaps 9;  
 QY 4 CPQGYIHPQNNISICTCKHKGTYLYNDCPGQDTPDCECESSGFTASENHLRHCLSCS 63  
 Db 32 CKDTET---KSHNLCLCLSCPPGTASRLCDSEK-TNTQCTPGSGGTFTSRNNHLPACLSCN 87  
 QY 64 -KCRKMGQVEISSCTVDRDTVCGCRKQYRHVWSENLFQCFNCSLCLNGT-VHLS 117  
 Db 88 GRCNS--NOVETRSQNTTHNRICRSPGY-----CLNGSSGCKACVAGT----- 131  
 QY 118 COEKONTVC-TCHAGFLRENECVS---CSNC-----KKSLECTKLCPLP 161  
 Db 132 -----KCGIGVGSGHVSVDVICSPCGFGYTSVSTKCEVFPVN 174  
 RESULT 14  
 T28623  
 C:Species: variola major virus  
 C/Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
 C/Accession: T28623  
 R/Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Uterback, T.R.; Knight, J.C.; Audi  
 Nature 366, 748-751, 1993  
 A>Title: Potential virulence determinants in terminal regions of variola smallpox virus  
 A/Reference number: Z20488; MUID:94088747; PMID:8264798  
 A/Accession: T28623  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-348 <MAS>



A; Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102  
A; Experimental source: strain Bangladesh 1975  
C; Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 164; DB 2; Length 348;  
Best Local Similarity 27.8%; Pred. No. 3.3e-05;  
Matches 42; Conservative 17; Mismatches 54; Indels 38; Gaps 8;

|  |    |    |   |     |
|--|----|----|---|-----|
|  | Qy | 4  | CPOGKYIHPPNNISICTKCHKHTYLYNDPCPGPDQDCECSGSFTASENHLRCLSCS    | 63  |
|  | :  | :  | : : : : :   | :   |
|  | Db | 31 | CKDTFY--KRHNLCCLSPGGYSARLCDSK-TNTQCTFCGSGTFTSRNNHLPACLSC    | 86  |
|  | :  | :  | : : : : :   | :   |
|  | Qy | 64 | -KCKEMGQVEISSCTSDVDRTVCGCRKNQRYHWSENLPQCF-----NCSLCINGTVHLS | 117 |
|  | :  | :  | : : : : :   | :   |
|  | Db | 87 | GRGNS--NOVETRSCTNTHRIICECPGYV-----CLLKGSNGCKACVSOT----      | 130 |
|  | :  | :  | : : : : :   | :   |

Qy 118 CQEKQNTVCTCHAGFFLRENECVS---CSNC 145  
                  |      |      |      |      |  
Db 131 -----KCGIGYGVSGHTSVGDVICSPC 152

RESULT 15  
D36858  
gene G4R protein - variola virus  
N:Alternate names: B28R protein (COP)  
C:Species: variola virus  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 23-Mar-2001  
C:Accession: D36858; S46888; S32385; S35987  
R:Blinov, V.M.  
submitted to GenBank, November 1992  
A:Reference number: A36859  
A:Accession: D36858  
A>Status: preliminary  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-349 <BLI>  
A:Cross-references: GB:X69198; NID:G456758; PIDN:CAA49137.1; PID:G457087  
A:Experimental source: strain India-1967, ssp. major, isolate Ind3  
R:Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, A.A.  
submitted to the EMBL Data Library, April 1992  
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P  
A:Reference number: S46868  
A:Accession: S46888  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-349 <RGL>  
A:Cross-references: EMBL:X67117; NID:G516428; PIDN:CAA47540.1; PID:G516449  
A:Experimental source: strain India-1967, isolate Ind3  
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.  
FEBS Lett. 319, 80-83, 1993  
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective  
A:Reference number: S32385; MUID:93202281; PMD:83844129

Query Match 17.4%; Score 164; DB 2; Length 349;  
Best Local Similarity 27.8%; Pred. No. 3.3e-05;  
Matches 42; Conservative 17; Mismatches 54; Indels 38; Gaps 8;

QY 4 CPOGKYIHPONNSICCTCKHKGTYLYNDGPGQDTCRECSGFTASENHLRCLSCS 63  
Db 32 CKDTEY---KRNLLCCLSPGTYASRLCDSK-TNQTCTPGSGTFTSRNNHLPACLSCN 87  
QY 64 -KCRKEMGQVEISSCTVDRTVCGCRKNQYRHYWSENLPQCF-----NCSLCLNCTVHLS 117



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OM protein - protein search, using sw model

Run on: December 3, 2002, 14:36:18 ; Search time 13 Seconds  
(without alignments)  
513.668 Million cell updates/sec

Title: US-09-907-263-2

Perfect score: 941

Sequence: 1 DSVCPQKGYHPQNNISICT.....CSNCKKSLCKLCPQIEN 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 941   | 100.0       | 455    | 1     | TR1A_HUMAN  |
| 2          | 716.5 | 76.1        | 461    | 1     | TR1A_PIG    |
| 3          | 680   | 72.3        | 454    | 1     | TR1A_MOUSE  |
| 4          | 674.5 | 71.7        | 471    | 1     | TR1A_BOVIN  |
| 5          | 669   | 71.1        | 461    | 1     | TR1A_RAT    |
| 6          | 200.5 | 21.3        | 176    | 1     | TR23_MOUSE  |
| 7          | 200.5 | 21.3        | 176    | 1     | TR12_HUMAN  |
| 8          | 198.5 | 21.1        | 180    | 1     | TR22_MOUSE  |
| 9          | 187.5 | 19.9        | 435    | 1     | TRN3_HUMAN  |
| 10         | 182.5 | 19.4        | 427    | 1     | TR16_HUMAN  |
| 11         | 181.5 | 19.3        | 417    | 1     | TR16_MOUSE  |
| 12         | 181   | 19.2        | 474    | 1     | TR1B_MOUSE  |
| 13         | 179.5 | 19.1        | 326    | 1     | VT2_SFVKA   |
| 14         | 178   | 18.9        | 325    | 1     | VT2_SFVKA   |
| 15         | 176.5 | 18.8        | 332    | 1     | TRN6_PIG    |
| 16         | 176.5 | 18.8        | 425    | 1     | TR16_RAT    |
| 17         | 167.5 | 17.8        | 289    | 1     | TRN5_MOUSE  |
| 18         | 167.5 | 17.8        | 415    | 1     | TRN3_MOUSE  |
| 19         | 167   | 17.7        | 269    | 1     | TRN5_BOVIN  |
| 20         | 166.5 | 17.7        | 323    | 1     | TRN6_BOVIN  |
| 21         | 166.5 | 17.7        | 323    | 1     | CRMB_CAMPS  |
| 22         | 164   | 17.4        | 349    | 1     | CRMB_VARY   |
| 23         | 164   | 17.4        | 351    | 1     | CRMB_COMPX  |
| 24         | 164   | 17.4        | 401    | 1     | T11B_HUMAN  |
| 25         | 162.5 | 17.3        | 327    | 1     | TRN6_MOUSE  |
| 26         | 161   | 17.1        | 461    | 1     | TR1B_HUMAN  |
| 27         | 158   | 16.8        | 401    | 1     | T11B_RAT    |
| 28         | 154   | 16.4        | 401    | 1     | T11B_MOUSE  |
| 29         | 147   | 15.6        | 324    | 1     | TRN6_RAT    |
| 30         | 145   | 15.4        | 416    | 1     | TR16_CHICK  |
| 31         | 142   | 15.1        | 283    | 1     | TR14_HUMAN  |
| 32         | 142   | 15.1        | 386    | 1     | T10D_HUMAN  |
| 33         | 141   | 15.0        | 1680   | 1     | FUR2_DROME  |

## ALIGNMENTS

### RESULT 1

| ID | TR1A_HUMAN   | STANDARD; | PRT; | 455 AA. |
|----|--|-----------|------|---------|
| AC | P19438;  |           |      |         |
| DT | 01-FEB-1991 (Rel. 17, Created)   |           |      |         |
| DT | 01-FEB-1991 (Rel. 17, Last sequence update)                            |           |      |         |
| DT | 15-JUN-2002 (Rel. 41, Last annotation update)                          |           |      |         |
| DE | Tumor necrosis factor receptor superfamily member 1A precursor (p60)   |           |      |         |
| DE | (TNF-R1) (TNF-RI) (p55) (CD120a) [Contains: Tumor necrosis factor      |           |      |         |
| DE | binding protein 1 (TFPI)]  |           |      |         |
| GN | TNFRSF1A OR TNFR1 OR TNFR.   |           |      |         |
| OS | Homo sapiens (Human).  |           |      |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |           |      |         |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.             |           |      |         |
| OX | NCBI_TaxID=9606;   |           |      |         |
| RN | [1]_TaxID=9606;  |           |      |         |
| RP | SEQUENCE FROM N.A.   |           |      |         |
| RC | TISSUE=Placenta;   |           |      |         |
| RA | Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,    |           |      |         |
| RA | Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V., |           |      |         |
| RT | "Molecular cloning and expression of a receptor for human tumor        |           |      |         |
| RT | necrosis factor.";   |           |      |         |
| RL | Cell 61:361-370(1990).   |           |      |         |
| RN | [2]  |           |      |         |
| RP | SEQUENCE FROM N.A.   |           |      |         |
| RX | MEDLINE=90235284; PubMed=2158862;                                      |           |      |         |
| RA | Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M.,         |           |      |         |
| RA | Tabuchi H., Lesslauer W.,  |           |      |         |
| RT | "Molecular cloning and expression of the human 55 kd tumor necrosis    |           |      |         |
| RT | factor receptor.";   |           |      |         |
| RL | Cell 61:351-359(1990).   |           |      |         |
| RN | [3]  |           |      |         |
| RP | SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.         |           |      |         |
| RX | MEDLINE=91006021; PubMed=1698610;                                      |           |      |         |
| RA | Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R.,           |           |      |         |
| RA | Aderka D., Holtmann H., Wallach D.;                                    |           |      |         |
| RT | "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA   |           |      |         |
| RT | for the type I TNF-R, cloned using amino acid sequence data of its     |           |      |         |
| RT | soluble form, encodes both the cell surface and a soluble form of the  |           |      |         |
| RT | receptor.";  |           |      |         |
| RL | EMBO J. 9:3269-3278(1990).   |           |      |         |
| RN | [4]  |           |      |         |
| RP | SEQUENCE FROM N.A.   |           |      |         |
| RX | MEDLINE=91090841; PubMed=1702293;                                      |           |      |         |
| RA | Himmeler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K., |           |      |         |
| RA | Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;            |           |      |         |
| RT | "Molecular cloning and expression of human and rat tumor necrosis      |           |      |         |
| RT | factor receptor chain (p60) and its soluble derivative, tumor          |           |      |         |
| RT | necrosis factor-binding protein.";                                     |           |      |         |
| RL | DNA Cell Biol. 9:705-715(1990).  |           |      |         |
| RN | [5]  |           |      |         |
| RP | SEQUENCE FROM N.A.   |           |      |         |
| RC | TISSUE=Placenta;   |           |      |         |
| RX | MEDLINE=91017509; PubMed=2170974;                                      |           |      |         |
| RA | Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;              |           |      |         |

P41272 mus musculus  
P25942 homo sapien  
O14798 h tumor nec  
P26842 homo sapien  
O14763 homo sapien  
Q9nj15 branchioeco  
Q04592 mus musculus  
P92127 giardia lam  
Q9epu5 mus musculus  
Q92824 homo sapien  
P47741 mus musculus  
P25445 homo sapien

34 139.5 14.8 250 1 TNR7\_MOUSE  
35 139.5 14.8 277 1 TNR5\_HUMAN  
36 139 14.8 259 1 T10C\_HUMAN  
37 138.5 14.7 260 1 TNR7\_HUMAN  
38 137 14.6 440 1 T10B\_HUMAN  
39 134 14.2 1696 1 PKK5\_BRACL  
40 134 14.2 1877 1 PKK5\_MOUSE  
41 133 14.1 687 1 VS41\_GIALA  
42 132.5 14.1 655 1 TR21\_MOUSE  
43 132 14.0 913 1 PKK5\_HUMAN  
44 131.5 14.0 272 1 TNR4\_MOUSE  
45 130.5 13.9 335 1 TNR6\_HUMAN

RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and  
RT expression of recombinant soluble TNF-binding protein.";  
RT Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92250049; PubMed=1315717;  
RA Fuchs P., Strehl S., Dworzak M., Himmeler A., Ambros P.F.;  
RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and  
RT localization to chromosome 12p13.";  
RL Genomics 13:219-224(1992).  
RN [7]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Muscle;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE OF 41-45.  
RX MEDLINE=90110215; PubMed=2153136;  
RA Engelmann H., Novick D., Wallach D.;  
RT "Two tumor necrosis factor-binding proteins purified from human  
RT urine. Evidence for immunological cross-reactivity with cell surface  
RT tumor necrosis factor receptors.";  
RL J. Biol. Chem. 265:11531-11536(1990).  
RN [9]  
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.  
RX MEDLINE=93258809; PubMed=8387891;  
RA Banner D.W., D'Arcy A., Janes W., Genz R., Schoenfeld H.-J.,  
RT Broger C., Loetscher H., Lesslauer N.;  
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
RT beta complex: implications for TNF receptor activation.";  
RL Cell 73:431-445(1993).  
RN [10]  
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
RX MEDLINE=97094982; PubMed=8939750;  
RA Naismith J.H., Devine T.Q., Khoro H., Sprang S.R.;  
RT "Structures of the extracellular domain of the type I tumor necrosis  
RT factor receptor.";  
RL Structure 4:1251-1262(1996).  
RN [11]  
RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.  
RX MEDLINE=99213501; PubMed=10199409;  
RA McDermott M.F., Aksentijevich I., Galon J., McDermott E.M.,  
RA Ogunkolade B.W., Centola M., Mansfield E., Gadiña M., Karenko L.,  
RA Petersen T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,  
RA Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,  
RA Schlingens R., Kumarajewa T.R., Cooper S.M., Vella J.P., Amos C.I.,  
RA Mulley U., Quane K.A., Molloy M.G., Rakki A., Powell R.J.,  
RA Hiltman G.A., O'Shea J., Kastner D.L.;  
RT "germline mutations in the extracellular domains of the 55 kDa TNF  
RT receptor, TNFR1, define a family of dominantly inherited  
RT autoinflammatory syndromes.";  
RL Cell 97:133-144(1999).  
CC -1- FUNCTION: Receptor for TNFR2/TNF-alpha and homotrimeric  
CC TNFR1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
CC caspase-8 to the activated receptor. The resulting death-inducing  
CC signaling complex (DISC) performs caspase-8 proteolytic activation  
CC which initiates the subsequent cascade of caspases (aspartate-  
CC specific cysteine proteases) mediating apoptosis. Contributes to  
CC the induction of noncytotoxic TNF effects including anti-viral  
CC state and activation of the acid sphingomyelinase.  
CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
CC NF-KAPPA B SIGNALING.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
CC -1- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO  
CC THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH  
CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.  
CC -1- PTM: The soluble form is produced from the membrane form by

CC proteolytic processing.  
CC -1- DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant  
CC familial hibernian fever (FHF), a disease characterized by  
CC recurrent fever, abdominal pain, localized tender skin lesions and  
CC myalgia.  
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X55313; CAA39021.1; -;  
CC DR EMBL; M33294; AAA03210.1; -;  
CC DR EMBL; M58286; AAA36753.1; -;  
CC DR EMBL; M63121; AAA36754.1; -;  
CC DR EMBL; M75866; AAA61201.1; -;  
CC DR EMBL; M75864; AAA61201.1; JOINED.  
CC DR EMBL; M75865; AAA61201.1; JOINED.  
CC DR EMBL; M60755; AAA36756.1; -;  
CC DR EMBL; A21522; CAA01558.1; -;  
CC DR EMBL; BC010140; AAH10140.1; -;  
CC DR PIR; A34899; G0HUT1.  
CC DR PIR; A35010; A35010.  
CC DR PIR; S12057; S12057.  
CC DR PIR; A38208; A38208.  
CC DR PDB; 1TNR; 31-JUL-94.  
CC DR PDB; 1NCF; 07-DEC-95.  
CC DR PDB; 1EXT; 11-JAN-97.  
CC DR Gene; HGNC:11916; TNFRSF1A.  
CC DR MIM; 191180; -;  
CC DR MIM; 142680; -;  
CC DR InterPro; IPR000488; Death.  
CC DR InterPro; IPR001368; TNFR\_c6.  
CC DR Pfam; PF00020; TNFR\_c6; 4.  
CC DR Pfam; PF00031; death; 1.  
CC DR ProDom; PD000771; TNFR\_c6; 1.  
CC DR SMART; SM00005; DEATH; 1.  
CC DR SMART; SM00208; TNFR; 4.  
CC DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
CC DR PROSITE; PS00500; TNFR\_NGFR\_2; 3.  
CC DR PROSITE; PS00017; DEATH\_DOMAIN; 1.  
CC DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;  
CC KW Disease mutation; Polymorphism; 3D-structure.  
CC FT CHAIN 1 21  
CC FT SIGNAL 1 21  
CC FT 22 455  
CC FT 21  
CC FT CHAIN 41 291  
CC FT DOMAIN 22 211  
CC FT TRANSMEM 212 234  
CC FT DOMAIN 235 455  
CC FT REPEAT 43 82  
CC FT REPEAT 83 125  
CC FT REPEAT 126 166  
CC FT REPEAT 167 196  
CC FT REPEAT 197 348  
CC FT DOMAIN 356 441  
CC FT DOMAIN 44 58  
CC FT DISULFID 59 72  
CC FT DISULFID 62 81  
CC FT DISULFID 84 99  
CC FT DISULFID 102 117  
CC FT DISULFID 105 125  
CC FT DISULFID 127 143  
CC FT DISULFID 146 158  
CC FT DISULFID 149 166  
CC FT DISULFID 168 179  
CC -----  
CC TUMOR NECROSIS FACTOR RECEPTOR  
CC SUPERFAMILY MEMBER 1A, MEMBRANE FORM.  
CC TUMOR NECROSIS FACTOR BINDING PROTEIN 1.  
CC EXTRACELLULAR (POTENTIAL).  
CC POTENTIAL.  
CC CYTOPLASMIC (POTENTIAL).  
CC TNFR-CYS 1.  
CC TNFR-CYS 2.  
CC TNFR-CYS 3.  
CC TNFR-CYS 4.  
CC N-SMASE ACTIVATION DOMAIN (NSD).  
CC DEATH.

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Query Match      100.0%; Score 941; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.2e-71;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISCTCKHKGTYLYNDPCPGQDTCRECSGFTASENHLRCL 60
DB 41 DSVCPQGYIHPQNNISCTCKHKGTYLYNDPCPGQDTCRECSGFTASENHLRCL 100

QY 61 SCSKCRKMGQVEISSCTVDRDTCGCRKNQVRYHWSNLFQCFNCSLCNGTVHLSQOE 120
DB 101 SCSKCRKMGQVEISSCTVDRDTCGCRKNQVRYHWSNLFQCFNCSLCNGTVHLSQOE 160

QY 121 KONTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 161
DB 161 KONTVCTCHAGFFLRENECVSCNCKSLECTKLCPLQIEN 201

RESULT 2
TRIA_PIG
ID TRIA_PIG STANDARD; PRT; 461 AA.
AC P50555;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN TNFRSF1A OR TNFR1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RC TISSUE=Kidney;
RA MEDLINE=96011645; PubMed=7590278;
RT Suter B., Pauli U.H.;
RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
RL Gene 163:263-266(1995).
CC -!- FUNCTION: Receptor for TNFSP2/TNF-alpha and homotrimeric
CC TNFSP1/lymphotoxin-alpha. The adaptor molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis (By similarity).
CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U19994; AAC48499.1; -.
DR HSSP; P19438; 1TNF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR Pfam; PF00531; death; 1.
DR ProDom; PD000771; TNFR_c6; 1.

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DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00552; TNFR_NGFR_1; 3.
DR PROSITE; PS00550; TNFR_NGFR_2; 2.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 461
FT DOMAIN 22 210
FT TRANSMEM 211 233
FT DOMAIN 234 461
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 195
FT DOMAIN 340 350
FT DOMAIN 362 447
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 194
FT DISULFID 185 190
FT CARBOHYD 54 54
FT CARBOHYD 86 86
FT CARBOHYD 145 145
FT CARBOHYD 151 151
SQ SEQUENCE 461 AA; 50696 MW; CD7361EC60C9D43 CRC64;

Query Match      76.1%; Score 716.5; DB 1; Length 461;
Best Local Similarity 77.4%; Pred. No. 5.8e-53;
Matches 120; Conservative 12; Mismatches 22; Indels 1; Gaps 1;

QY 1 DSVCPQGYIHPQNNISCTCKHKGTYLYNDPCPGQDTCRECSGFTASENHLRCL 60
DB 41 ESLCPQGYIHPQNNISCTCKHKGTYLYNDPCPGQDTCRECSGFTASENHLRCL 100

QY 61 SCSKCRKMGQVEISSCTVDRDTCGCRKNQVRYHWSNLFQCFNCSLCNGTVHLSQOE 120
DB 101 SCSKCRKMGQVEISSCTVDRDTCGCRKNQVRYHWSNLFQCFNCSLCNGTVHLSQOE 160

QY 121 KONTVCTCHAGFFLRENECVSCNCKSLECTKLC 155
DB 161 KODTICNCHSGFFLRDKCEVCNCKNA-DCKNLC 194

RESULT 3
TRIA_MOUSE
ID TRIA_MOUSE STANDARD; PRT; 454 AA.
AC P25118;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RA MEDLINE=9118785; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor

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RT necrosis factor receptors demonstrate one receptor is species specific.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).  
 RN (2)  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=91246168; PubMed=1645445;  
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,  
 RA Copeland N.G., Jenkins N.A., Smith C.A.;  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 RT receptors for tumor necrosis factor.";  
 RT Mol. Cell. Biol. 11:3020-3026 (1991).  
 RN (3)  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=91285014; PubMed=1647956;  
 RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Klesonerghis A.M.,  
 RA Gray P.W., Feldmann M., Foxwell B.M.J.;  
 RT "Cloning, expression and cross-linking analysis of the murine p55  
 RT tumor necrosis factor receptor.";  
 RT Eur. J. Immunol. 21:1649-1656 (1991).  
 RN (4)  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=SpLeen;  
 RX MEDLINE=92039815; PubMed=1657766;  
 RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;  
 RT "Molecular cloning and expression of the mouse Tnf receptor type b.";  
 RT Immunogenetics 34:338-340 (1991).  
 RN (5)  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=94245292; PubMed=8188324;  
 RA Bebo B.F., Linthicum D.S.;  
 RT "Nucleotide sequence of the TNF type I receptor from a mouse  
 RT endometrialoma cell line.";  
 RT Immunogenetics 39:450-451 (1994).  
 RN (6)  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=93156721; PubMed=8381515;  
 RA Rothe J., Bluthmann H., Gentz R., Lesslauer W., Steinmetz M.;  
 RT "Genomic organization and promoter function of the murine tumor  
 RT necrosis factor receptor beta gene.";  
 RT Mol. Immunol. 30:165-175 (1993).  
 RN (7)  
 RN SEQUENCE FROM N.A.  
 RA Strauberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
 CC TNFSF2/Lymphotoxin-alpha. The adaptor molecule FADD recruits  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC specific cysteine proteases) mediating apoptosis (by similarity).  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC  
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 CC  
 CC EMBL; M50468; AAA39751.1; -;  
 DR EMBL; M59377; AAA40464.1; -;  
 DR EMBL; X59238; CAA41922.1; -;

DR EMBL; X57796; CAA40936.1; -;  
 DR EMBL; L26349; AAA59361.1; -;  
 DR EMBL; M76656; AAA40465.1; -;  
 DR EMBL; M88067; AAA40465.1; JOINED.  
 DR EMBL; M76655; AAA40465.1; JOINED.  
 DR EMBL; BC004599; AA04599.1; -;  
 DR PIR; A38634; GQMSLT.  
 DR PIR; S16677; S16677.  
 DR PIR; S19021; S19021.  
 DR HSSP; P19438; IEXT.  
 DR MGD; MGI:131484; Tnfalfa.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR Pfam; PF00531; death; 1.  
 DR ProDom; PD000771; TNFR\_c6; 1.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 KW SIGNAL  
 FT CHAIN 1 21  
 FT 22 454  
 FT  
 FT DOMAIN 22 212  
 FT TRANSMEM 213 235  
 FT DOMAIN 236 454  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 196  
 FT DOMAIN 339 349  
 FT DOMAIN 356 441  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
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 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 195  
 FT DISULFID 185 191  
 FT CARBOHYD 54  
 FT CARBOHYD 151 151  
 FT CARBOHYD 202 202  
 FT CONFLICT 394  
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 Query Match 72.3%; Score 680; DB 1; Length 454;  
 Best Local Similarity 71.3%; Pred. No. 6,2e-50;  
 Matches 112; Conservative 19; Mismatches 26; Indels 0; Gaps 0;  
 QY 1 DSVCPQGVYHPPNNNSICTYCHKGTLYNDPQPGQDTDCREESGFSFASENHLRCL 60  
 Db 41 DDLCPQGVKSHKNNISICTYCHKGTLYVSDPSGRDVCRECEKGTFTASQVLYRCL 100  
 QY 61 SCSKRKEGVETSSCTVDBDVTGCGKKNQYHMYWSNLFQCNCSLCLNGTHTLSOE 120  
 Db 101 SKTKRKESQVETSPCADKDTVCGCKENQFORLSTHFQCVDCSPFNGVTYIPCKE 160  
 QY 121 KONTVCTCHAGFFLRENECVSCNCKSLCTKTLCLP 157  
 Db 161 TONTVONCHAGFFLRESECVPSHCKNKECKMLCLP 197  
 RESULT 4  
 TRIA\_BOVIN  
 ID TRIA\_BOVIN  
 AC O19131;  
 STANDARD; PRT; 471 AA.

DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
 DE (TNF-R1) (TNF-R1) (p55).  
 GN TNFRSF1A OR TNFR1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Aorta;  
 RX MEDLINE=98273505; PubMed=9613449;  
 RA Lee E.-K., Kehrl M.E. Jr., Taylor M.J.;  
 RT "Cloning and sequencing of cDNA encoding bovine tumor necrosis factor  
 (TNF)-receptor 1";  
 RL Vet. Immunol. Immunopathol. 61:379-385(1998).  
 CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
 CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
 CC caspase-8 to the activated receptor. The resulting death-inducing  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC specific cysteine proteases) mediating apoptosis (By similarity).  
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.  
 CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
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 CC  
 CC -----  
 CC EMBL; U0937; AAB65143.1; -.  
 CC HSP; P19438; 1TNR.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR Pfam; PF00531; death; 1.  
 DR ProDom; PD000771; TNFR\_c6; 1.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS00017; DEATH DOMAIN; 1.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 471 TUMOR NECROSIS FACTOR RECEPTOR  
 FT SUPERFAMILY MEMBER 1A.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TNFR-CYS 1.  
 FT TNFR-CYS 2.  
 FT TNFR-CYS 3.  
 FT TNFR-CYS 4.  
 FT N-SMASE ACTIVATION DOMAIN (NSD).  
 FT DEATH.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81

FT DISULFID 84 99 BY SIMILARITY.  
 FT DISULFID 102 117 BY SIMILARITY.  
 FT DISULFID 105 125 BY SIMILARITY.  
 FT DISULFID 127 143 BY SIMILARITY.  
 FT DISULFID 146 158 BY SIMILARITY.  
 FT DISULFID 149 166 BY SIMILARITY.  
 FT DISULFID 168 179 BY SIMILARITY.  
 FT DISULFID 182 194 BY SIMILARITY.  
 FT DISULFID 185 190 BY SIMILARITY.  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 471 AA; 5243EP514DFE81C4 CRC64;  
 Query Match 71.7%; Score 674.5; DB 1; Length 471;  
 Best Local Similarity 71.6%; Pred. No. 1.8e-49;  
 Matches 111; Conservative 17; Mismatches 26; Indels 1; Gaps 1;  
 QY 1 DSVCPQGYTHPONNSICTCKCHKGTLYLNDPCGQDTCRECESGSFTASENHLRCL 60  
 DB 41 ESPCPQGYNHPPQNSICTCKCHKGTLYLNDPCGQDTCRCVCAPTVALENHURCL 100  
 QY 61 SCCKRCKEMQVSEISSCTVDRTVCCGRKNQRYHWSNLFQCFNCSLCLNGTVHLSCOE 120  
 DB 101 SCGRCDPMFQVEISPCWDRDTCVCCGRKNQRYEYWGTFGRCLNCSLCPNGTVNIPQE 160  
 QY 121 KONTVCTCHAGFTLRENECVSCNCKKSLCTKLC 155  
 DB 161 RQDTICHCHMGFFLGKACISCHDCKNK-ECEKLC 194  
 RESULT 5  
 TRIA-RAT  
 ID TRIA-RAT STANDARD; PRT; 461 AA.  
 AC P22934; Q91V30; Q91Y93;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
 DE (TNF-R1) (TNF-R1) (p55).  
 GN TNFRSF1A OR TNFR1 OR TNFR-1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91090841; PubMed=1702293;  
 RA Himmler A., Maurer-Pogoy I., Kroenke M., Scheurich P., Pfizenmaier K.,  
 RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;  
 RT "Molecular cloning and expression of human and rat tumor necrosis  
 RT factor receptor chain (p60) and its soluble derivative, tumor  
 RT necrosis factor-binding protein.";  
 RL DNA Cell Biol. 9:705-715(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND VARIANTS VAL-230 AND PRO-295.  
 RC STRAIN=Various;  
 RA Furuya T., Saistrom J.L., Bina J., Hashimoto A., Dobbins D.E.,  
 RA Wilder R.L., Remmers E.F.;  
 RT "Polymorphisms of the tumor necrosis factor receptor type 1 locus  
 RT among autoimmune susceptible and resistant inbred rat strains.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
 CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
 CC caspase-8 to the activated receptor. The resulting death-inducing  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC specific cysteine proteases) mediating apoptosis (By similarity).  
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO

|    |   |   |
|----|---|---|
|    | C   | TNR-RELATED PROTEIN.  |
|    | C   | -1- SUBCELLULAR LOCATION: Type I membrane protein.  |
|    | C   | -1- SIMILARITY: CONTAINS 4 TNR-CYS REPEATS.   |
|    | C   | -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  |
|    | C   | -- --   |
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|    | C   | -- --   |
|    | D   | EMBL; M63122; AAA42256.1; -. .  |
|    | D   | EMBL; AF389796; AAK53562.1; -. .  |
|    | D   | EMBL; AF389797; AAK53563.1; -. .  |
|    | D   | EMBL; AF389981; AAK53567.1; -. .  |
|    | D   | EMBL; AF389978; AAK53564.1; -. .  |
|    | D   | EMBL; AF389979; AAK53565.1; -. .  |
|    | D   | EMBL; AF389980; AAK53566.1; -. .  |
|    | D   | PIR; B36555; B36555. .  |
|    | D   | HSPD; P19438; INCF. .   |
|    | D   | InterPro: IPRO00489; Death. .   |
|    | D   | InterPro: IPRO01368; TNFR_c6. .   |
|    | D   | Pfam; PF00020; TNFR_c6; 4_ .  |
|    | D   | Pfam; PF00531; death; 1_ .  |
|    | D   | Prodcm; PD000771; TNFR_c6; 1_ .   |
|    | D   | SMART; SMO0208; TNFR; 3_ .  |
|    | D   | PROSITE; PS00652; TNFR_NGFR_1; 3_ .   |
|    | D   | PROSITE; PS00650; TNFR_NGFR_2; 3_ .   |
|    | D   | PROSITE; PS0017; DEATH_DOMAIN; 1_ .   |
|    | KW  | Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.   |
|    | FT  | SIGNAL  |
|    | FT  | CHAIN   |
|    | FT  | DOMAIN  |
|    | FT  | TRANSMEM  |
|    | FT  | REPEAT  |
|    | FT  | REPEAT  |
|    | FT  | REPEAT  |
|    | FT  | REPEAT  |
|    | FT  | DOMAIN  |
|    | FT  | DISULFID  |
|    | FT  | DISULFID  |
|    | FT  | DISULFID  |
|    | FT  | DISULFID  |
|    | FT  | DISULFID  |
|    | FT  | DISULFID  |
|    | FT  | DISULFID  |
|    | FT  | DISULFID  |
|    | FT  | DISULFID  |
|    | FT  | CARBOHYD  |
|    | FT  | VARIANT   |
|    | FT  | VARIANT   |
|    | SEQENCE   | SEQUENCE  |
|    | BEST LOCAL  | Best Local Similarity   |
|    | MATCHES   | Matches   |
| QY | 1 DSVCGKGIHQNNSICTCKCHKGYLVINDCGRPGPDITDCRCBSGSFTASENHLRHCL | Score 669; DB 1; Length 461;<br>Pred. No. 5,2e+49;<br>Mismatches 33; Indels 0; Gaps 0;  |

|   |  |     |   |     |
|---|--|-----|---|-----|
| D6  |  | 41  | DNLCPGKKYAPRKNKNSICCTCKHGGTYLVSDPCSPGQETVCEVDCKPTFASQNHVRQCL    | 100 |
| OY  |  | 61  | SCSKCRKEMGVVEISSCTVDRDVTVCGRKNOYRHYSBNLFOCNCSLCNGTVHLSQOE       | 120 |
| D6  |  | 101 | SKCTCRKEMGFVEIISPCCADMDPVGCGKKNOFCORYLTSETHFGQCDCSPPCFNGTYPICKE | 160 |
| OY  |  | 121 | KONTVCTCHAGGFLEBNCVSCSNCKSLCETKTLCLQOIEH                        | 161 |
| D6  |  | 161 | KONTVCTCHAGGFPLSGNECTPCHSHCKXNQBCKMLCLPVPAN                     | 201 |
| <br>RESULT 6<br>TR23_MOUSE STANDARD; PRT; 176 AA. |  |     |   |     |
| ID  | _TR23_MOUSE  |     |   |     |
| AC  | QSER63; Q8VHC0;  |     |   |     |
| DT  | 15-JUN-2002 (Rel. 41, Created)   |     |   |     |
| DT  | 15-JUN-2002 (Rel. 41, Last sequence update)  |     |   |     |
| DT  | 15-JUN-2002 (Rel. 41, Last annotation update)  |     |   |     |
| DE  | Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis   |     |   |     |
| GN  | factor receptor p60 homolog 1) (TNF receptor family member SOB).   |     |   |     |
| OS  | TNFRSF23 OR TNFRSF1A1 OR TNFRH1.   |     |   |     |
| OC  | Mus musculus (Mouse).  |     |   |     |
| OX  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |     |   |     |
| CC  | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.   |     |   |     |
| NB  | NCBI_TaxId=10090;  |     |   |     |
| RN  | [1]  |     |   |     |
| RP  | SEQUENCE FROM N.A.   |     |   |     |
| RC  | STRAIN=129/Sv; TISSUE=Embryonic stem cells;  |     |   |     |
| RX  | MEDLINE=20519229; PubMed=11063728;   |     |   |     |
| RA  | Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,   |     |   |     |
| RT  | Lane N., Reik W., Walter J.;   |     |   |     |
| RL  | "Sequence and functional comparison in the Beckwith-Wiedemann region:  |     |   |     |
| RP  | implications for a novel imprinting centre and extended imprinting.";  |     |   |     |
| RN  | Hum. Mol. Genet. 9:2691-2706(2000).  |     |   |     |
| RR  | [2]  |     |   |     |
| RA  | SEQUENCE FROM N.A.   |     |   |     |
| RT  | Pan G., Mao W., Risser P.;   |     |   |     |
| RL  | "Characterization of SOB, a member of the TNFR family.";   |     |   |     |
| CC  | Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  |     |   |     |
| CC  | -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  |     |   |     |
| CC  | -1- TISSUE SPECIFICITY: Ubiquitous.  |     |   |     |
| CC  | -1- SIMILARITY: CONTAINS 3 TNFR-CVS REPEATS.   |     |   |     |
| CC  | -----  |     |   |     |
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| CC  | entities requires a license agreement (See <a href="http://www.isb.ch/announce/">http://www.isb.ch/announce/</a> ) |     |   |     |
| CC  | or send an email to <a href="mailto:license@isb.ch">license@isb.ch</a> .   |     |   |     |
| CC  | -----  |     |   |     |
| DR  | EMBL; AJ278264; CAC16405.1; -  |     |   |     |
| DR  | EMBL; AJ276505; CAC27352.1; -  |     |   |     |
| DR  | EMBL; AY046550; AAL05072.1; -  |     |   |     |
| DR  | HSSP: PL9438; TEXT.  |     |   |     |
| DR  | MGP; MG1:1930269; Tnfrcsf23.   |     |   |     |
| DR  | InterPro; IPR001368; TNFR_C6.  |     |   |     |
| DR  | Pfam; PF00202; TNFR_C6; 3.   |     |   |     |
| DR  | SMART; PF00208; TNFR_3.  |     |   |     |
| KW  | PROSITE; PS0050; TNFR_NGFR_2; 2.   |     |   |     |
| FT  | Receptor; Signal_anchor; Transmembrane; Glycoprotein; Repeat.  |     |   |     |
| FT  | DOMAIN   | 1   | 9   |     |
| FT  | TRANSMEM   | 10  | 30  |     |
| FT  | (CYTOPLASMIC (POTENTIAL))  |     |   |     |
| FT  | SIGNAL_ANCHOR (TYPE II MEMBRANE PROTEIN)   |     |   |     |
| FT  | (POTENTIAL).   |     |   |     |
| FT  | DOMAIN   | 31  | 176   |     |
| FT  | REPEAT   | 37  | 72  |     |
| FT  | EXTRACELLULAR (POTENTIAL).   |     |   |     |
| FT  | TNFR_CVS 1.  |     |   |     |
| FT  | REPEAT   | 74  | 114   |     |
| FT  | TNFR_CVS 2.  |     |   |     |
| FT  | TNFR_CVS 3.  |     |   |     |
| FT  | REPEAT   | 115 | 155   |     |
| FT  | TNFR_CVS 3.  |     |   |     |
| FT  | DISULFD  | 38  | 49  |     |
| FT  | BY SIMILARITY.   |     |   |     |
| FT  | DISULFD  | 50  | 63  |     |
| FT  | BY SIMILARITY.   |     |   |     |
| FT  | DISULFD  | 53  | 72  |     |
| FT  | BY SIMILARITY.   |     |   |     |
| FT  | DISULFD  | 75  | 90  |     |
| FT  | BY SIMILARITY.   |     |   |     |



Curr. Biol. 6:1669-1676(1996).

[5] SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10). MEDLINE=9727273; PubMed=9114039;

XX Sreaton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,

RA McMichael A.J., Bell J.I.;

RT "LARD: a new lymphoid-specific death domain containing receptor

RT regulated by alternative pre-mRNA splicing.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).

[6] SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).

RP MEDLINE=98113360; PubMed=9446802;

RA Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,

RT Salles G.;

RA "A new death receptor 3 isoform: expression in human lymphoid cell

RT lines and non-Hodgkin's lymphomas.";

RL Biochem. Biophys. Res. Commun. 242:376-379(1998).

[7] SEQUENCE FROM N.A. (ISOFORM 1).

RP Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto E.,

RA Hayaishi S., Sato M., Shiozawa K., Tsukamoto Y.;

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

[8] SEQUENCE OF 4-417 FROM N.A.

RP TISSUE=Brain, and Fetal lung;

RC MEDLINE=97205335; PubMed=9052839;

RA Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,

RA Thome M., Bornand T., Hahne M.R., Schroeter M., Wilson A., French L.E.,

RA Browning J.L., Macdonald H.R., Tschoopp J.;

RT "TRAMP, a novel apoptosis-mediating receptor with sequence homology

RT to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";

RL Immunity 6:79-88(1997).

[9] SEQUENCE OF 7-417 FROM N.A.

RP TISSUE=Brain;

RC Chaudhary P.M., Hood L.E.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Receptor for TNFSGF12/AP03L/TWEAK. Interacts directly

CC with the adaptor TRADD. Mediates activation of NF-kappaB and

CC induces apoptosis. May play a role in regulating lymphocyte

CC homeostasis.

CC -!- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH

CC THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNFR1 RECEPTOR TO

CC ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND

CC NF-KAPPA B SIGNALING.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9

CC and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)

CC (Potential).

CC -!- ALTERNATIVE PRODUCTS: 12 ISOFORMS; 1/WSL-1/LARD-1A (SHOWN HERE),

CC 2/LARD-1B, 3/WSL-S1/LARD-3, 4/WSL-S2/LARD-2, 5/LARD-4/LARD-11,

CC 6/LARD-5, 7/LARD-6, 8/LARD-7, 9/LARD-8, 10/LARD-9, 11/BETA AND

CC 12/BETA SOLUBLE; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND

CC LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,

CC COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.

CC -!- PTM: GLYCOSYLATED (PROBABLE).

CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

CC -!- CAUTION: Ref:5 reports for isoform 4 at position 208 a serine

CC residue instead of arginine.

-----

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EMBL; Y09392; CAA70561.1; -

DR EMBL; Y09392; CAA70559.1; -

DR EMBL; Y09392; CAA70560.1; -

DR EMBL; U72763; AAC50819.1; -





|  |             |   |
|--|-------------|---|
|  | CC          | associated cell death executor.   |
|  | CC          | -1 SUBCELLULAR LOCATION: Type I membrane protein.   |
|  | CC          | -1-PTM: N- AND O-glycosylated.  |
|  | CC          | -1-PTM: Phosphorylated on serine residues.  |
|  | CC          | -1 SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.   |
|  | CC          | -1 SIMILARITY: CONTAINS 1 DEATH DOMAIN.   |
|  | CC          | -----   |
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|  | CC          | or send an email to license@isb-sib.ch).  |
|  | CC          | EMBL; M14764; AA859544.1; -.  |
|  | DR          | EMBL; M21621; AAA36363.1; -.  |
|  | DR          | PIR; A25218; GOHUN.   |
|  | DR          | HSSP; P07174; INGR.   |
|  | DR          | Genew; HGNC:1809; NGFR.   |
|  | DR          | MIM; 162010; -.   |
|  | DR          | InterPro; IPRO00488; Death.   |
|  | DR          | InterPro; IPRO01368; TNFR_c6.   |
|  | DR          | Pfam; PF00020; TNFR_c6; 4.  |
|  | DR          | Pfam; PF00531; death; 1.  |
|  | DR          | SMART; SMO0005; DEATH; 1.   |
|  | DR          | SMART; SMO0208; TNFR; 3.  |
|  | DR          | PROSITE; PS00652; TNFR_NGFR_1, 3.   |
|  | DR          | PROSITE; PS50050; TNFR_NGFR_2, 4.   |
|  | DR          | PROSITE; PS50017; DEATH_DOMAIN; 1.  |
|  | KW          | Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;   |
|  | KW          | Repeat; Phosphorylation; signal.  |
|  | FT          | SIGNAL  |
|  | FT          | CHAIN   |
|  | FT          | DOMAIN  |
|  | FT          | TRANSMEM  |
|  | FT          | DOMAIN  |
|  | FT          | REPEAT  |
|  | FT          | REPEAT  |
|  | FT          | REPEAT  |
|  | FT          | REPEAT  |
|  | FT          | DOMAIN  |
|  | FT          | DOMAIN  |
|  | FT          | DISULFID  |
|  | FT          | DISULFID  |
|  | FT          | DISULFID  |
|  | FT          | DISULFID  |
|  | FT          | DISULFID  |
|  | FT          | DISULFID  |
|  | FT          | DISULFID  |
|  | FT          | DISULFID  |
|  | FT          | DISULFID  |
|  | FT          | DISULFID  |
|  | FT          | CARBOHYD  |
|  | FT          | SEQUENCE  |
|  | SO          | SEQUENCE  |
|  | Query Match | Best Local Similarity 32.1%; Pred. No. 1,6e-08; Matches 52; Conservative 25; Mismatches 62; Indels 23; Gaps 11  |
|  | QY          | 4 CPQGYIHPNNISICTCKHKGTLYINDCPGPQDTDCREC-ESGSFTASENHLRHCLSC 62  |
|  | Dd          | 32 CPTGLVTH---SSECKKACNLGEVAQC-GANQ-TVCEPLCDVTSTVDVSATPECKPC 86   |
|  | QY          | 63 SKCRKMGQVEIIS-CTVDRDYVCCKRKNOVRHWSENLPCCFNCSICLNGT-VHLSQOE 120   |
|  | Dd          | 87 TEC---VGLOSMAPCVEADDAVRCRC--AVGYODETTGGCEACRCVCAAGSGLVFSOD 140   |
|  | QY          | 121 KONTVC-TCHAGFLAE-----NECVSCSNC-----KKSLCTKC 153   |

Db 141 KONTVCECPDGTYSDEANHVDPCLPCTVCTEDTERQLRECTR 182

RESULT 11

TR16 MOUSE

ID TR16 MOUSE STANDARD; PRT; 417 AA.

AC Q920W1;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-affinity nerve growth factor receptor) (NGF receptor) (Low affinity neurotrophin receptor p75NTR).

DE NGFR OR TNFRSF16.

GN Mus musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI\_TaxID=10090;

OX [1]\_TaxID=10090;

RN

RP SEQUENCE FROM N.A.

RC STRAIN=A;

RX MEDLINE=99077793; PubMed=9857182;

RA Tuffreau C., Benejean J., Blondel D., Kieffer B., Flamand A.;

RT "Low-affinity nerve growth factor receptor (p75NTR) can serve as a receptor for rabies virus.";

RL EMBO J. 17:7250-7259(1998).

CC -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3, and NT-4. Can mediate cell survival as well as cell death of neural cells (By similarity). Binds to rabies virus glycoprotein Gs.

CC -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-associated cell death executor (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- PTM: N- AND O-glycosylated (By similarity).

CC -!- PTM: Phosphorylated on serine residues (By similarity).

CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

CC

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CC

DR EMBL; AF105292; AAD17943.1; ..

DR HSP; P07174; INGR.

DR MGP; MGI:97323; Ngfr.

DR InterPro; IPR000486; Death.

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00531; death; 1.

DR Pfam; PF00020; TNFR\_c6; 4.

DR SMART; SM00005; DEATH; 1.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.

DR PROSITE; PS00050; TNFR\_NGFR\_2; 4.

DR PROSITE; PS00017; DEATH\_DOMAIN; 1.

DR Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein; Repeat; Signal.

DR SIGNAL 1 21 BY SIMILARITY.

DR CHAIN 22 417 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 16.

FT DOMAIN 22 246 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 247 265 POTENTIAL.

FT DOMAIN 266 417 CYTOPLASMIC (POTENTIAL).

FT REPEAT 24 57 TNFR-CYS 1.

FT REPEAT 59 100 TNFR-CYS 2.

FT REPEAT 101 139 TNFR-CYS 3.

FT REPEAT 141 181 TNFR-CYS 4.

FT DOMAIN 190 241 DEATH.

FT DOMAIN 190 241 SER/THR-RICH.

FT DISULFID 25 36 BY SIMILARITY.

FT DISULFID 37 50 BY SIMILARITY.

FT DISULFID 40 57 BY SIMILARITY.

FT DISULFID 60 76 BY SIMILARITY.

FT DISULFID 79 92 BY SIMILARITY.

FT DISULFID 82 100 BY SIMILARITY.

FT DISULFID 102 115 BY SIMILARITY.

FT DISULFID 118 131 BY SIMILARITY.

FT DISULFID 121 139 BY SIMILARITY.

FT DISULFID 142 157 BY SIMILARITY.

FT DISULFID 160 173 BY SIMILARITY.

FT DISULFID 163 181 BY SIMILARITY.

FT CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).

SQ SEQUENCE 417 AA; 44686 MW; 5D7A4510D8AF9B2 CRC64;

Query Match 19.3%; Score 181.5; DB 1; Length 417;

Best Local Similarity 31.5%; Pred. No. 1.9e-08;

Matches 51; Conservative 25; Mismatches 67; Indels 19; Gaps 10;

QY 4 CPOGKIHPQNNISCTCKHGTLYNDGPGQDQDDCREC-ESGSFTASENHLRHCLSC 62

DB 25 CSTGMVTH---SGECCACNKGVAQPC-GANQ-TVCEPCLDSVTFSVDVSGATEPKFC 79

QY 63 SKCRKEMGQVEISS-CTVDRDVTVCGRKNQRYHWSENLFQCFNCSLCLNGT-VHLSQCE 120

DB 80 TEC---LGLQSMAPCVAEADDAVCRC---SYGYQDEETGRCEACSVCGVSGSLVFSCQD 133

QY 121 KONTVC-TCHAGFFLE---NECVSCSNCKSKLECTKCLCP 157

DB 134 KONTVCECPGTYSDEANHVDPCLPCTVCTEDTERQLRECTP 175

RESULT 12

TR16 MOUSE

ID TR16 MOUSE STANDARD; PRT; 474 AA.

AC P25119; P97893;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor necrosis factor receptor 2) (TNF-R2) (p75).

GN TNFRSF1B OR TNFR2 OR TNFR-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]\_TaxID=10090;

RP SEQUENCE FROM N.A.

RX MEDLINE=91187885; PubMed=1849278;

RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,

RA Wong G.H., Chen E.Y., Goeddel D.V.;

RT "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.";

RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=91246168; PubMed=1645445;

RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,

RA Copeland N.G., Jenkins N.A., Smith C.A.;

RT "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.";

RT Mol. Cell. Biol. 11:3020-3026(1991).

RN [3]

RP SEQUENCE OF 1-26 FROM N.A.

RN [4]

RP STRAIN=NOB;

RC STRAIN=NOB;

RA Jacob C.O., Liu J.;

RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

RP TISSUE=Liver;

RC TISSUE=Liver;

RA Kisonerghis M., Fellows R., Feldmann M., Chernajovsky Y.;

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and



```

FT REPEAT 27 62 TNFR-CYS 1.
FT REPEAT 63 104 TNFR-CYS 2.
FT REPEAT 105 147 TNFR-CYS 3.
FT REPEAT 148 186 TNFR-CYS 4.
FT DISULFID 28 39 BY SIMILARITY.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 43 61 BY SIMILARITY.
FT DISULFID 64 79 BY SIMILARITY.
FT DISULFID 82 96 BY SIMILARITY.
FT DISULFID 86 104 BY SIMILARITY.
FT DISULFID 106 120 BY SIMILARITY.
FT DISULFID 123 146 BY SIMILARITY.
FT DISULFID 129 149 BY SIMILARITY.
FT DISULFID 164 185 BY SIMILARITY.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;

Query Match 18.9%; Score 178; DB 1; Length 325;
Best Local Similarity 29.8%; Pred. No. 3e-08;
Matches 45; Conservative 15; Mismatches 62; Indels 30; Gaps 6;

QY 13 QNNSICCTCKHGTYLYNDPCGQDQDCRECSGSPASENHLRHLCLSC-SKCRKEMGQ 71
: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 34 EKDLCCASCHPGFYASRLC-GPGSNTVCSPCEDGTFTASTNHAPACVSCRGPCTGHLs- 91
: : : : : : : : : : : : : : : : : : : : : : : : : :

QY 72 VEISSCTVDRDTVCGGRKNQRYHWSENLPQCNCSLCLNGTVHLSQCEKQNTVCTCHAG 131
: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 92 -ESQPCDRTHDRVNCNSTGNYCLLKQN-----GCRICAPQT-----KCPAG 132
: : : : : : : : : : : : : : : : : : : : : : : : : :

QY 132 FFLRENECVSCSNCKK-----SLECTKLC 155
: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 133 YGVSHTRAGDTLCEKCPHPHTYSDLSLSPTEPC 164
: : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
TNR6 PIG
ID TNR6 PIG STANDARD; PRT; 332 AA.
AC Q7736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT "Expression of apoptosis-associated genes in hibernating and stunned
RL myocardium of pig.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (by similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
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CC -----  
 DR EMBL: AJ001202; CAA04596.1; -  
 DR HSP: P25445; 1DDF.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001358; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 3.  
 DR Pfam: PF00531; death; 1.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00208; TNFR; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS00500; TNFR\_NGFR\_2; 2.  
 DR PROSITE: PS00177; DEATH\_DOMAIN; 1.  
 DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 16  
 FT CHAIN 17 332  
 FT DOMAIN 17 175  
 FT TRANSMEM 176 192  
 FT DOMAIN 193 332  
 FT REPEAT 45 81  
 FT REPEAT 82 125  
 FT REPEAT 126 164  
 FT DOMAIN 227 311  
 FT DISULFID 46 57  
 FT DISULFID 58 71  
 FT DISULFID 61 80  
 FT DISULFID 83 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 141  
 FT DISULFID 144 155  
 FT DISULFID 147 163  
 FT CARBOHYD 38 38  
 FT CARBOHYD 116 116  
 SQ SEQUENCE 332 AA; 37592 MW; 5B8B03682756BF1B CRC64;

Query Match 18.8; Score 176.5; DB 1; Length 332;

Best Local Similarity 29.1; Pred. No. 4.1e-08; Indels 7; Gaps 4;  
 Matches 37; Conservative 18; Mismatches 65;

QY 1 DSVDPGKYIHPNNSICTCKHGTLYLNDPCPGQDTDCRECESG-SFTASENHLRHC 59  
 Db 43 ESECPGQH--RSGQFTCPCPGPKRHADCTSPGAPQCVPSBSEDYTDKNHSSKC 99  
 QY 60 LSCSKCKREMGQVEISSCTVDRTVCGCKNQYRHWSENLFQCFNCSLCINGTHLSQ 119  
 Db 100 RRCVDCDEHGLEVEKNTKTRQNTKCRCKPFFCH--TSQCEHCNPCTCEHGVIE-NCT 156  
 QY 120 EKQNTVC 126  
 Db 157 PTSNTKC 163

Search completed: December 3, 2002, 14:40:24  
 Job time : 15 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 3, 2002, 14:38:48 ; Search time 31 Seconds  
(without alignments)  
1070.116 Million cell updates/sec

Title: US-09-907-263-2

Perfect score: 941

Sequence: 1 DSVCFQGYIHPQNNISICT.....CSNCKSLEKTLCLPQIEN 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_viridap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID     | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 780   | 82.9        | 446    | 6 Q95ND3  | Q95nd3 felis silve |
| 2          | 756   | 80.3        | 189    | 6 Q97530  | Q97530 canis fami  |
| 3          | 731   | 77.7        | 189    | 6 Q95185  | Q95185 felis silve |
| 4          | 202   | 21.5        | 413    | 11 Q99MM1 | Q99mm1 mus musculu |
| 5          | 193   | 20.5        | 387    | 11 Q9PVD4 | Q9pvd4 xenopus lae |
| 6          | 191   | 20.3        | 433    | 11 Q91ZM6 | Q91zm6 rattus norv |
| 7          | 188   | 20.0        | 302    | 13 Q9DGH7 | Q9dgh7 gallus gall |
| 8          | 182.5 | 19.4        | 285    | 13 Q9DGH7 | Q9dgh8 gallus gall |
| 9          | 179.5 | 19.1        | 357    | 13 Q9DF34 | Q9df34 brachydanio |
| 10         | 176.5 | 18.8        | 320    | 12 Q57079 | Q57079 cowpox viru |
| 11         | 176   | 18.7        | 459    | 11 Q62327 | Q62327 mus musculu |
| 12         | 175.5 | 18.7        | 312    | 13 Q9DGH8 | Q9dgh8 gallus gall |
| 13         | 175.5 | 18.7        | 322    | 12 Q72761 | Q72761 cowpox viru |
| 14         | 171.5 | 18.2        | 316    | 12 Q57092 | Q57092 ectromelia  |
| 15         | 171.5 | 18.2        | 320    | 12 Q57091 | Q57091 ectromelia  |
| 16         | 171.5 | 18.2        | 320    | 12 Q57300 | Q57300 ectromelia  |

|    |       |      |     |    |        |                      |
|----|-------|------|-----|----|--------|----------------------|
| 17 | 171.5 | 18.2 | 482 | 11 | Q88734 | Q88734 mus musculu   |
| 18 | 169   | 18.0 | 326 | 12 | Q57120 | Q57120 cowpox viru   |
| 19 | 168   | 17.9 | 347 | 12 | Q57119 | Q57119 cowpox viru   |
| 20 | 168   | 17.9 | 351 | 12 | Q57121 | Q57121 cowpox viru   |
| 21 | 167.5 | 17.8 | 349 | 12 | Q57100 | Q57100 monkeypox v   |
| 22 | 167   | 17.7 | 326 | 12 | Q57122 | Q57122 cowpox viru   |
| 23 | 167   | 17.7 | 347 | 12 | Q57115 | Q57115 cowpox viru   |
| 24 | 166.5 | 17.7 | 349 | 12 | Q57098 | Q57098 camelpox vi   |
| 25 | 166.5 | 17.7 | 349 | 12 | Q57111 | Q57111 variola vir   |
| 26 | 166.5 | 17.7 | 349 | 12 | Q8UYA7 | Q8UYA7 camelpox vi   |
| 27 | 166.5 | 17.7 | 349 | 12 | Q89098 | Q89098 variola vir   |
| 28 | 166.5 | 17.7 | 349 | 12 | Q57284 | Q57284 camelpox vi   |
| 29 | 166   | 17.6 | 360 | 12 | Q57118 | Q57118 camelpox viru |
| 30 | 165   | 17.5 | 277 | 6  | Q8WMQ2 | Q8wmq2 ovis aries    |
| 31 | 165   | 17.5 | 349 | 12 | Q57109 | Q57109 variola vir   |
| 32 | 164.5 | 17.5 | 348 | 12 | Q57103 | Q57103 monkeypox v   |
| 33 | 164.5 | 17.5 | 348 | 12 | Q57108 | Q57108 monkeypox v   |
| 34 | 164.5 | 17.5 | 348 | 12 | Q57277 | Q57277 monkeypox v   |
| 35 | 164   | 17.4 | 348 | 12 | Q57112 | Q57112 variola vir   |
| 36 | 164   | 17.4 | 348 | 12 | Q85407 | Q85407 variola vir   |
| 37 | 164   | 17.4 | 349 | 12 | Q57110 | Q57110 variola vir   |
| 38 | 164   | 17.4 | 349 | 12 | Q89118 | Q89118 variola vir   |
| 39 | 164   | 17.4 | 351 | 12 | Q73559 | Q73559 cowpox viru   |
| 40 | 162.5 | 17.3 | 349 | 12 | Q57099 | Q57099 monkeypox v   |
| 41 | 162.5 | 17.3 | 349 | 12 | Q57101 | Q57101 monkeypox v   |
| 42 | 162.5 | 17.3 | 349 | 12 | Q57102 | Q57102 monkeypox v   |
| 43 | 162.5 | 17.3 | 349 | 12 | Q57291 | Q57291 monkeypox v   |
| 44 | 162   | 17.2 | 349 | 12 | Q57305 | Q57305 cowpox viru   |
| 45 | 162   | 17.2 | 350 | 12 | Q57123 | Q57123 cowpox viru   |

## ALIGNMENTS

RESULT 1

Q95ND3 PRELIMINARY; PRT; 446 AA.  
AC Q95ND3;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Tumor necrosis factor type I.  
GN TNFR I.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;  
RT "Molecular cloning of feline tumor necrosis factor receptor type I  
RT (TNFR I) and expression of TNFR I and TNFR II in various disease in  
RT cats.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB051103; BAB55455.1; -.  
DR InterPro; IPR000345; CytC\_heme\_bind.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR SMART; SM00181; EGF\_1.  
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN\_1.  
DR PROSITE; PS0017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_3.  
DR PROSITE; PS00500; TNFR\_NGFR\_2; 3.  
SQ SEQUENCE 446 AA; 49563 MW; 217BD331DD8A74AA CRC64;

Query Match 82.9%; Score 780; DB 6; Length 446;  
Best Local Similarity 84.1%; Pred. NO. 1.5e-78;  
Matches 132; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 4 CPOGKYIHPONNSICCTKCHKGTLYLYNDCEPGQDTCRECESSGFTASBNHLRHCLSCS 63  
 DB 44 CPOGKYIHPONNSICCTKCHKGTLYLYNDCEPGQDTCRECESSGFTASBNHLRHCLSCS 103  
 QY 64 KCRKEMGVVEISCTVDRDTCGCRKNQRYRYWSETHFQCLNCSLCLNGTVQISCKEON 123  
 DB 104 KCRKEMGVVEISCTVDRDTCGCRKNQRYRYWSETHFQCLNCSLCLNGTVQISCKEON 163  
 QY 124 TVCTCHAGFPLRNECVSCSNCKSLCTCLCPOIE 160  
 DB 164 TVCTCHAGFPLRNECVSCSNCKSLCTCLCPOIE 200

## RESULT 2

ID 097530 PRELIMINARY; PRT; 189 AA.  
 AC 097530;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Tumour necrosis factor receptor p60 (Fragment).  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 RN NCBI\_TaxID=9615;  
 RX MEDLINE=21109092; PubMed=1182158;  
 RA Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthie S.,  
 Bennett D.;  
 RT "Cloning of canine IL-1ra, TNFR and TNF-2";  
 RL Vet. Immunol. Immunopathol. 78:207-214(2001).  
 DR EMBL; AF013955; AAD01516.1; -.  
 DR HSSP; P19438; 1TNR.  
 DR InterPro; IPR000561; EGF-like.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 KM Receptor.  
 SQ SEQUENCE 189 AA; 21324 MW; 5D3AD6A5676BF399 CRC64;

Query Match 80.3%; Score 756; DB 6; Length 189;  
 Best Local Similarity 87.0%; Pred. No. 3e-76;  
 Matches 127; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 3 VCPGKYIHPONNSICCTKCHKGTLYLYNDCEPGQDTCRECESSGFTASBNHLRHCLSC 62  
 DB 43 VCPGKYIHPONNSICCTKCHKGTLYLYNDCEPGQDTCRECESSGFTASBNHLRHCLSC 102  
 QY 63 KCRKEMGVVEISCTVDRDTCGCRKNQRYRYWSETHFQCLNCSLCLNGTVQISCKEON 122  
 DB 103 KCRKEMGVVEISCTVDRDTCGCRKNQRYRYWSETHFQCLNCSLCLNGTVQISCKEON 162  
 QY 123 NTVCTCHAGFPLRNECVSCSNCKKS 148  
 DB 163 NTVCTCHAGFPLRNECVSCSNCKKS 188

## RESULT 3

ID 095185 PRELIMINARY; PRT; 189 AA.  
 AC 095185;  
 DT 01-FEB-1997 (TREMBlrel. 02, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Tumour necrosis factor receptor p60 (Fragment).  
 GN TNFR-1.  
 OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 RN NCBI\_TaxID=9685;  
 RX MEDLINE=9685;  
 RA Duthie S., Nasir L., Ekersall P.D.;  
 RT "Felis catus tumour necrosis factor receptor p60 (TNFR-1) mRNA,  
 partial cds.";  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U72344; AAB95089.1; -.  
 DR HSSP; P19438; 1EXT.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 KM Receptor.  
 SQ SEQUENCE 189 AA; 21420 MW; F3FBE0CE809D7DBE CRC64;

Query Match 77.7%; Score 731; DB 6; Length 189;  
 Best Local Similarity 85.5%; Pred. No. 1.8e-73;  
 Matches 124; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 4 CPOGKYIHPONNSICCTKCHKGTLYLYNDCEPGQDTCRECESSGFTASBNHLRHCLSCS 63  
 DB 44 CPOGKYIHPONNSICCTKCHKGTLYLYNDCEPGQDTCRECESSGFTASBNHLRHCLSCS 103  
 QY 64 KCRKEMGVVEISCTVDRDTCGCRKNQRYRYWSETHFQCLNCSLCLNGTVQISCKEON 123  
 DB 104 KCRKEMGVVEISCTVDRDTCGCRKNQRYRYWSETHFQCLNCSLCLNGTVQISCKEON 163  
 QY 124 TVCTCHAGFPLRNECVSCSNCKKS 148  
 DB 164 TVCTCHAGFPLRNECVSCSNCKKS 188

## RESULT 4

ID 099MM1 PRELIMINARY; PRT; 413 AA.

AC 099MM1;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE WSL-1-like protein.  
 GN TNFRSF12.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 RX MEDLINE=11261933; PubMed=11261933;  
 RA Wang E.C.Y., Kiteon J., Thern A., Williamson J., Farrow S.N.,  
 Owen M.J.;  
 RT "Genomic structure, expression, and chromosome mapping of the mouse  
 homologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12)  
 gene.";  
 RL Immunogenetics 53:59-63(2001).  
 DR EMBL; AF329969; AAK11256.1; -.  
 DR HSSP; P25942; 1CDF.  
 DR MGD; MGI:193467; Tnf1sf12.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.

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RESULT 7
Q9PUS0
ID Q9PUS0 PRELIMINARY; PRT; 302 AA.
OC Q9PUS0;
DT DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Decoy TNF receptor.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
[1]
RN
SEQUENCE FROM N.A.
RP MEDLINE=20111091; PubMed=10642582;
RA Robe J., Goetz F.W.;
RX "A tumor necrosis factor decoy receptor homologue is up-regulated in
RT the brook trout (Salvelinus fontinalis) ovary at the completion of
RT ovulation."
RL Biol. Reprod. 62:420-426(2000).
RL EMBL; AF156738; AAD56428.1; -.
DR HSSP; O14763; 1DAV.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.

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RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF296874; AAG02242.1; -  
DR HSP; 014763; IDAV.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
DR NON TER 1  
SQ SEQUENCE 312 AA; 35275 MW; 5496BCF1E4CE676C CRC64;

Query Match 18.7%; Score 175.5; DB 13; Length 312;  
Best Local Similarity 32.7%; Pred. No. 1.6e-11;  
Matches 36; Conservative 14; Mismatches 55; Indels 5; Gaps 3;

QY 18 CCTKCHKTYLYNDPCPGODTDCRECSG-SPTASENHLRHCLSCSKCKREMGQVEISS 76  
DB 6 CCTKCKRHVKSIDC-EKTOAHCVPRKSGEYMDHINDLDECMRCSCKALGLEVYKN 63  
QY 77 CTVDRTVCGCRKNQYRHVWSENLFQCFNCSCLNGTVHLSQCKONTVC 126  
DB 64 CTSTENACSCAKNHYCN--SSRCEHCECTVCENGQIEKCTSTDTVC 111

RESULT 13  
ID 072761 PRELIMINARY; PRT; 322 AA.  
AC 072761

DT 01-AUG-1998 (TRENBLrel. 07, Created)  
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)  
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE K2R protein.  
GN K2R.

OS Cowpox virus (CPV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_Taxid=10243;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GRI-90;  
RX MEDLINE=98229462; Pubmed=9568042;  
RA Shchelkunov S.N., Safironov P.F., Tocmenin A.V., Petrov N.A.,  
RA Ryzankina O.I., Guttorov V.V., Kotwal G.J.;  
RT "Species-specific differences in genome organization of cowpox,  
RT smallpox, and vaccinia viruses";  
RL Virology 243:432-460(1998).

DR EMBL; Y15035; CAAT5300.1; -  
DR HSP; 014763; IDOG.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_2.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
SQ SEQUENCE 322 AA; 35412 MW; 774549278D156A9D CRC64;

Query Match 18.7%; Score 175.5; DB 12; Length 322;  
Best Local Similarity 27.7%; Pred. No. 1.6e-11;  
Matches 41; Conservative 22; Mismatches 60; Indels 25; Gaps 6;

QY 7 GKYTHPONNSICTKCHKTYLYNDPCPGODTDCRECSGSPFASENHLRHCLSC-SKC 65  
DB 33 GTDYNSSNNLCKQCPGMYMTHSC-NTSNTKCAKCPDPTFTSIINHPTCLSCGKGC 91  
QY 66 RKEGQVEISSCTVDRTVCGCRKNQYRHVWSENLFQCFNCSCLNGTVHLSQCKONTVC 125  
DB 92 --SSNQVETSSCNTQRECVCAAGYCEFEFGSN-----GRLCVPT----- 132

QY 126 CTGAGFFL--RENECVSCNCKSL 150

DB 133 -KDCSGYGYGYSKQDVICKKCPGNID 159

RESULT 14  
ID 057092 PRELIMINARY; PRT; 316 AA.  
AC 057092

DT 01-JUN-1998 (TRENBLrel. 06, Created)  
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)  
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE Tumor necrosis factor receptor II homolog.  
GN CRMD.

OS Ectromelia virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_Taxid=12643;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MUNICH-SF(SILVER FOX);  
RX MEDLINE=98188282; Pubmed=9520445;  
RA Loparev V.N., Parsons J.M., Knight J.C., Panus J.F., Ray C.A.,  
RA Buller R.M.L., Pickup D.J., Esposito J.J.;  
RT "A third distinct tumor necrosis factor receptor of orthopoxviruses";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:3786-3791(1998).

DR EMBL; U87580; AAB94350.1; -  
DR HSP; P19438; TEXT.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
KW Receptor.  
SQ SEQUENCE 316 AA; 34660 MW; 443CC1185B4E12A9 CRC64;

Query Match 18.2%; Score 171.5; DB 12; Length 316;  
Best Local Similarity 27.8%; Pred. No. 4.4e-11;  
Matches 42; Conservative 22; Mismatches 62; Indels 25; Gaps 6;

QY 14 NNSICTKCHKTYLYNDPCPGODTDCRECSGSPFASENHLRHCLSC-SKCKREMGQV 72  
DB 34 SNLCKQCPGMYMTHSC-NTSNTKCDKCPDPTFTSIPIHSPACLSCKGK--SSNQV 90  
QY 73 EISCTVDRTVCGCRKNQYRHVWSENLFQCFNCSCLNGTVHLSQCKONTVC 132  
DB 91 ETKSSNTQDRVCAAGYCEFEFGSN-----GRLCVPT-----KCSGY 132  
QY 133 FL--RENECVSCNCKSLCKTCLPQIE 160  
DB 133 GYGYSSKQDVICKKCPGNIDKCLSFNSID 163

RESULT 15  
ID 057091 PRELIMINARY; PRT; 320 AA.  
AC 057091

DT 01-JUN-1998 (TRENBLrel. 06, Created)  
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)  
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE Tumor necrosis factor receptor II homolog.  
GN CRMD.

OS Ectromelia virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_Taxid=12643;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MUNICH-MF3;  
RX MEDLINE=98188282; Pubmed=9520445;  
RA Loparev V.N., Parsons J.M., Knight J.C., Panus J.F., Ray C.A.,  
RA Buller R.M.L., Pickup D.J., Esposito J.J.;  
RT "A third distinct tumor necrosis factor receptor of orthopoxviruses";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:3786-3791(1998).  
DR EMBL; U87578; AAB94348.1; -



